



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 12:14 PM EDT

PDB ID : 1VRN / pdb_00001vrn
Title : PHOTOSYNTHETIC REACTION CENTER BLASTOCHLORIS VIRIDIS (ATCC)
Authors : Baxter, R.H.G.; Seagle, B.-L.; Norris, J.R.
Deposited on : 2005-02-23
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

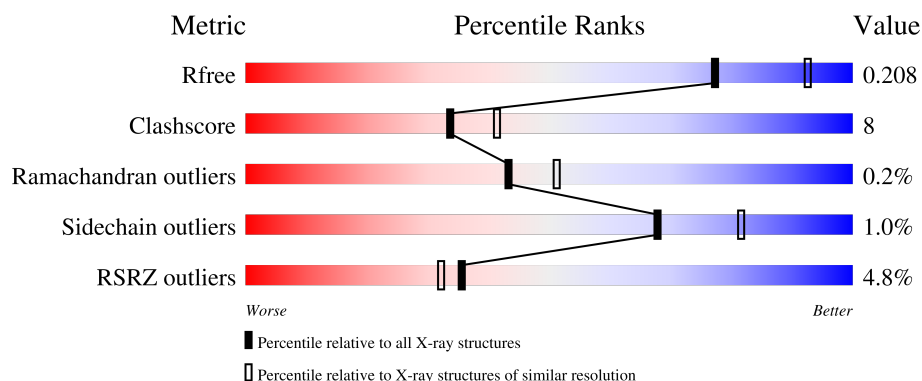
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

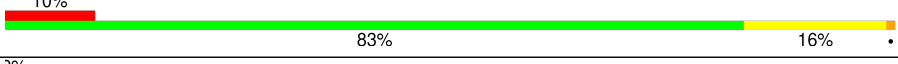
The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C	332	
2	H	258	
3	L	273	
4	M	323	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	HEC	C	401	X	-	-	-
5	HEC	C	402	X	-	-	-
5	HEC	C	403	X	-	-	-
5	HEC	C	404	X	-	-	-
6	SO4	H	807	-	-	X	-
8	BCB	L	402	X	-	-	-
8	BCB	L	404	X	-	-	-
8	BCB	M	401	X	-	-	-
8	BCB	M	403	X	-	-	-
9	BPB	M	405	X	-	-	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 10747 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Photosynthetic reaction center cytochrome c subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	332	Total	C	N	O	S	24	0	0
			2603	1640	466	479	18			

- Molecule 2 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	258	Total	C	N	O	S	112	0	0
			2018	1292	344	380	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	1	FME	MET	modified residue	UNP P06008

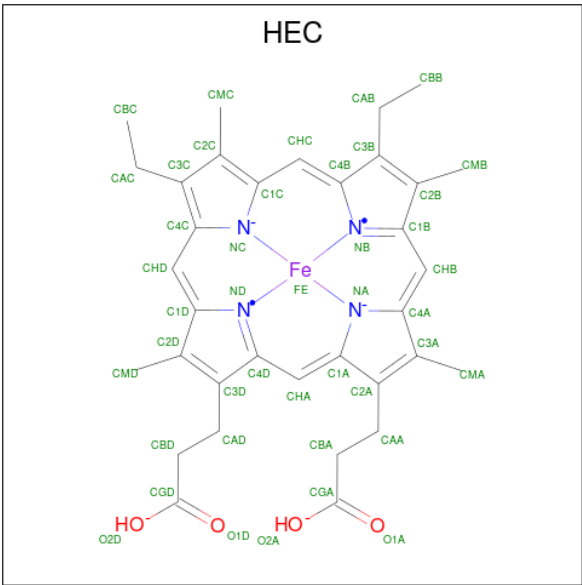
- Molecule 3 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	273	Total	C	N	O	S	5	1	0
			2177	1462	351	357	7			

- Molecule 4 is a protein called Reaction center protein M chain.

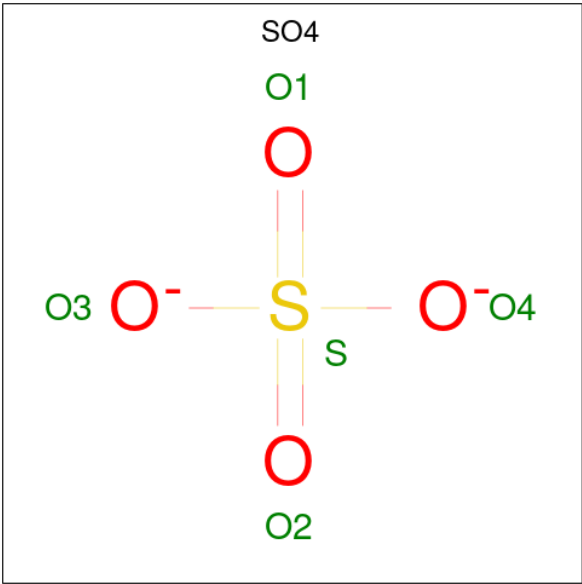
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	M	323	Total	C	N	O	S	10	1	0
			2563	1707	420	424	12			

- Molecule 5 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



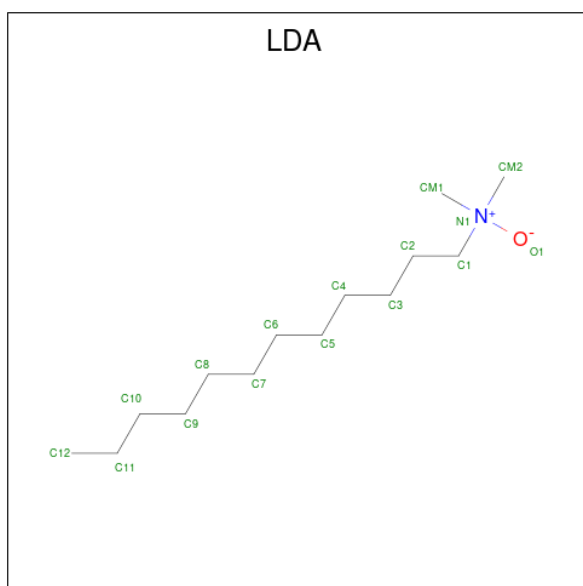
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	1	Total O S 5 4 1	0	0
6	H	1	Total O S 5 4 1	0	0
6	H	1	Total O S 5 4 1	0	0
6	M	1	Total O S 5 4 1	0	0
6	M	1	Total O S 5 4 1	0	0
6	M	1	Total O S 5 4 1	0	0
6	M	1	Total O S 5 4 1	0	0

- Molecule 7 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: C₁₄H₃₁NO).



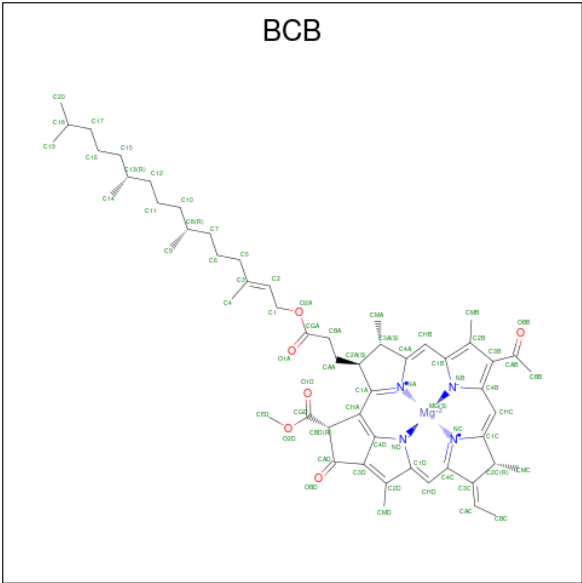
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	H	1	Total C N O 16 14 1 1	0	0
7	H	1	Total C N O 16 14 1 1	0	0
7	L	1	Total C N O 16 14 1 1	0	0
7	L	1	Total C N O 16 14 1 1	0	0
7	M	1	Total C N O 16 14 1 1	0	0

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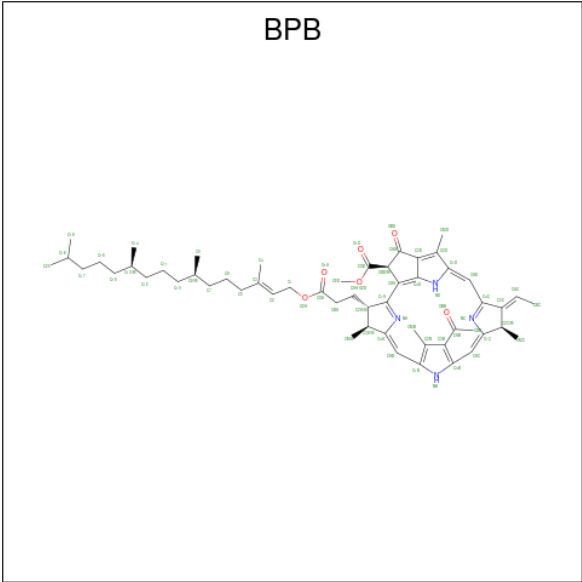
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	M	1	Total	C	N	O	4	0
			16	14	1	1		

- Molecule 8 is BACTERIOCHLOROPHYLL B (CCD ID: BCB) (formula: C₅₅H₇₂MgN₄O₆).



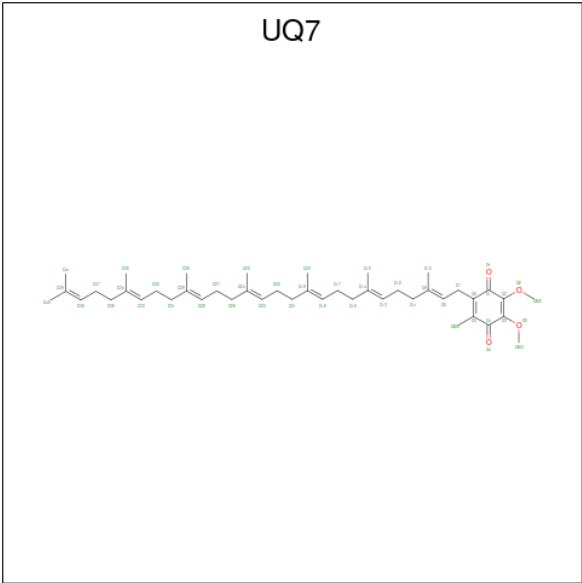
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	M	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	M	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

- Molecule 9 is BACTERIOPHEOPHYTIN B (CCD ID: BPB) (formula: C₅₅H₇₄N₄O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	L	1	Total	C	N	O	0	0
			65	55	4	6		
9	M	1	Total	C	N	O	9	0
			65	55	4	6		

- Molecule 10 is UBIQUINONE-7 (CCD ID: UQ7) (formula: C₄₄H₆₆O₄).

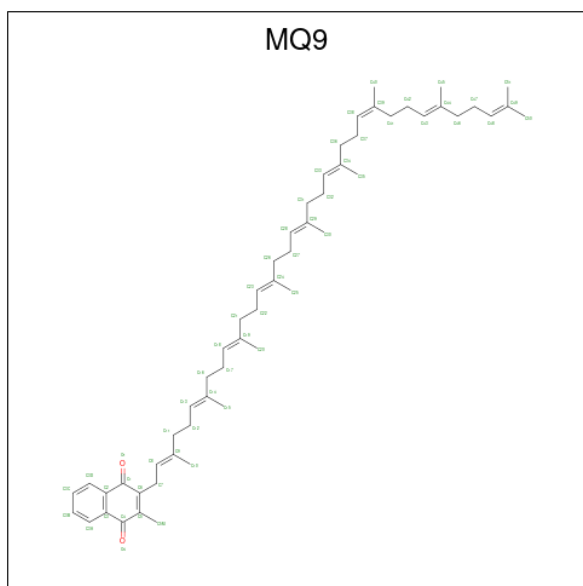


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	L	1	Total	C	O	0	0
			48	44	4		

- Molecule 11 is FE (II) ION (CCD ID: FE2) (formula: Fe).

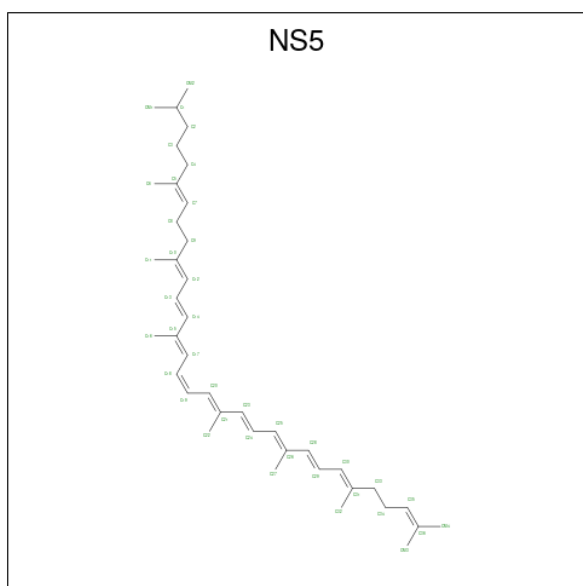
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	M	1	Total	Fe	0	0
			1	1		

- Molecule 12 is MENAQUINONE-9 (CCD ID: MQ9) (formula: $C_{56}H_{80}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	1	Total	C	O	0	0
			58	56	2		

- Molecule 13 is 15-cis-1,2-dihydroneurosporene (CCD ID: NS5) (formula: $C_{40}H_{60}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	M	1	Total C 40 40	0	0

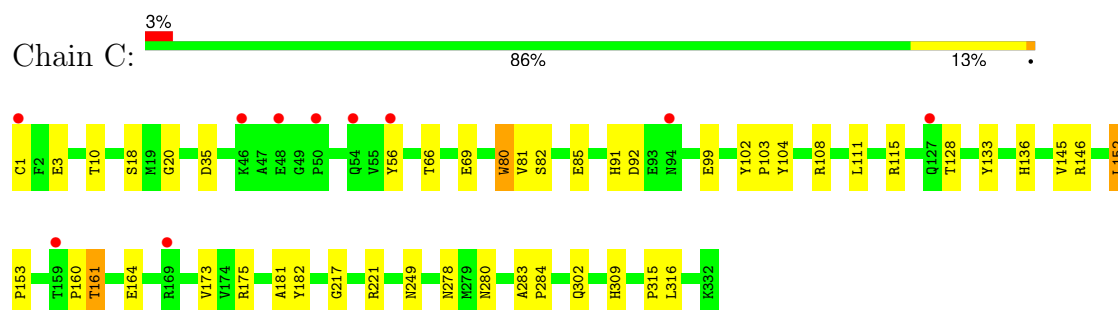
- Molecule 14 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	C	212	Total O 212 212	0	0
14	H	124	Total O 124 124	0	0
14	L	92	Total O 92 92	0	0
14	M	114	Total O 114 114	0	0

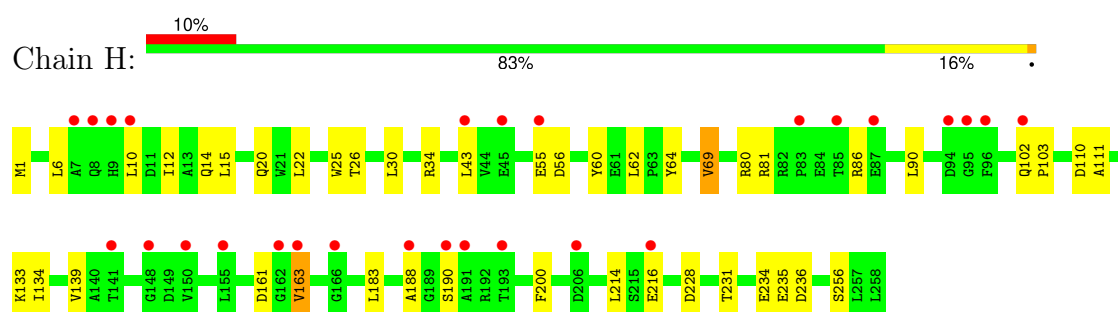
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

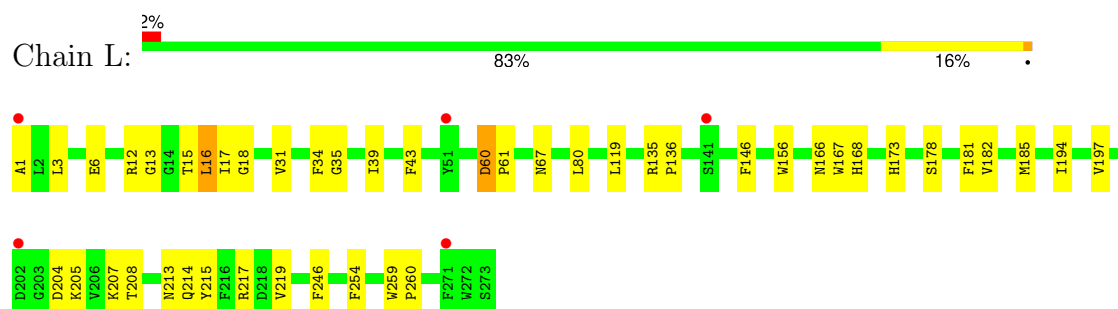
- Molecule 1: Photosynthetic reaction center cytochrome c subunit



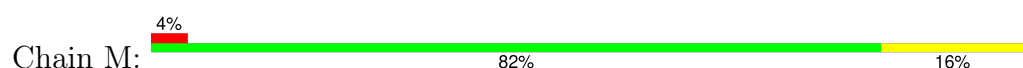
- Molecule 2: Reaction center protein H chain

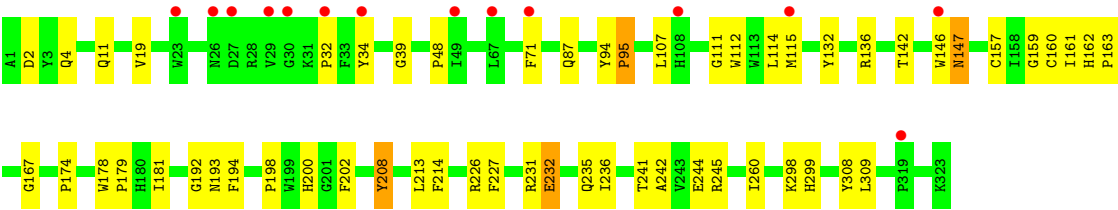


- Molecule 3: Reaction center protein L chain



- Molecule 4: Reaction center protein M chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	219.40Å 219.40Å 112.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.18 – 2.20 19.18 – 2.20	Depositor EDS
% Data completeness (in resolution range)	86.2 (19.18-2.20) 86.2 (19.18-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.15 (at 2.19Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.191 , 0.212 0.187 , 0.208	Depositor DCC
R_{free} test set	6079 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10747	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCB, HEC, SO4, FE2, BPB, UQ7, NS5, FME, MQ9, LDA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C	0.39	0/2670	0.93	10/3637 (0.3%)
2	H	0.35	0/2055	0.84	2/2807 (0.1%)
3	L	0.42	0/2265	0.94	8/3092 (0.3%)
4	M	0.40	0/2667	0.90	10/3647 (0.3%)
All	All	0.39	0/9657	0.90	30/13183 (0.2%)

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	200	HIS	N-CA-C	-9.04	101.50	111.36
1	C	249	ASN	N-CA-C	-8.31	93.99	108.20
3	L	6	GLU	N-CA-C	7.12	120.45	111.69
4	M	309	LEU	N-CA-C	-7.06	99.76	110.07
3	L	67	ASN	N-CA-C	6.79	119.21	110.39
4	M	94	TYR	N-CA-C	6.76	119.18	110.39
4	M	308	TYR	N-CA-C	-6.57	102.70	111.96
1	C	92	ASP	N-CA-C	-6.46	98.68	108.96
1	C	81	VAL	N-CA-C	6.43	117.78	111.67
1	C	221	ARG	N-CA-C	-6.25	102.18	109.93
4	M	244	GLU	N-CA-C	-6.11	104.70	111.36
4	M	208	TYR	N-CA-C	-6.07	104.67	111.28
4	M	95	PRO	N-CA-C	-6.06	103.31	110.70
2	H	12	ILE	N-CA-C	6.01	116.19	110.42
1	C	91	HIS	N-CA-C	5.85	119.25	109.95
3	L	208	THR	N-CA-C	5.79	117.39	109.18
1	C	80	TRP	N-CA-C	5.51	117.37	111.36
3	L	3	LEU	N-CA-C	-5.48	103.25	110.43
4	M	232	GLU	N-CA-C	5.24	116.99	111.28
1	C	161	THR	N-CA-C	-5.23	103.78	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	13	GLY	N-CA-C	5.22	117.37	112.04
1	C	136	HIS	N-CA-C	5.20	117.03	111.36
1	C	128	THR	N-CA-C	-5.20	105.05	111.40
4	M	213	LEU	N-CA-C	5.14	116.88	111.28
4	M	235	GLN	N-CA-C	-5.14	105.75	112.23
2	H	183	LEU	N-CA-C	-5.10	101.56	109.72
3	L	16	LEU	N-CA-C	-5.08	106.77	113.12
1	C	280	ASN	N-CA-C	5.08	119.62	113.38
3	L	60	ASP	CA-C-N	5.03	125.06	119.32
3	L	60	ASP	C-N-CA	5.03	125.06	119.32

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2603	0	2579	24	0
2	H	2018	0	2020	38	0
3	L	2177	0	2102	34	0
4	M	2563	0	2460	43	0
5	C	172	0	120	1	0
6	H	15	0	0	2	0
6	M	20	0	0	1	0
7	H	32	0	62	8	0
7	L	32	0	62	4	0
7	M	32	0	62	5	0
8	L	132	0	144	6	0
8	M	132	0	144	12	0
9	L	65	0	74	6	0
9	M	65	0	74	7	0
10	L	48	0	66	9	0
11	M	1	0	0	0	0
12	M	58	0	80	2	0
13	M	40	0	60	4	0
14	C	212	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	H	124	0	0	1	0
14	L	92	0	0	1	0
14	M	114	0	0	1	0
All	All	10747	0	10109	154	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (154) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:M:32:PRO:HG3	4:M:48:PRO:HD3	1.46	0.95
9:L:406:BPB:HHC	9:L:406:BPB:HBBB	1.52	0.92
9:M:405:BPB:HHC	9:M:405:BPB:HBBB	1.56	0.87
4:M:114:LEU:HG	13:M:600:NS5:HM43	1.64	0.79
2:H:69:VAL:HG13	3:L:205:LYS:HA	1.66	0.78
8:M:401:BCB:HBB2	8:M:401:BCB:HHC	1.66	0.77
1:C:152:LEU:HD22	1:C:175:ARG:HA	1.66	0.76
2:H:102:GLN:OE1	3:L:12:ARG:HD3	1.91	0.71
10:L:502:UQ7:H171	8:M:401:BCB:H91	1.73	0.70
4:M:71:PHE:HB3	7:M:705:LDA:H61	1.75	0.68
3:L:181:PHE:HB3	9:M:405:BPB:HBBA	1.74	0.68
3:L:214:GLN:NE2	4:M:19:VAL:H	1.91	0.68
1:C:153:PRO:HD3	1:C:160:PRO:HB3	1.77	0.67
9:L:406:BPB:HHC	9:L:406:BPB:CBB	2.24	0.66
2:H:86:ARG:NH2	2:H:111:ALA:HB3	2.11	0.65
8:M:401:BCB:H102	8:M:401:BCB:H142	1.77	0.65
2:H:69:VAL:HG12	14:H:1292:HOH:O	1.95	0.64
10:L:502:UQ7:H153	8:M:401:BCB:H101	1.78	0.64
2:H:81:ARG:H	7:H:703:LDA:H112	1.63	0.64
3:L:178:SER:HB3	10:L:502:UQ7:H261	1.79	0.64
9:L:406:BPB:HBBA	4:M:208:TYR:HB3	1.80	0.63
7:L:702:LDA:H72	7:L:702:LDA:H31	1.81	0.62
4:M:231:ARG:HD2	14:M:1383:HOH:O	1.98	0.62
3:L:181:PHE:CD2	9:M:405:BPB:HBB	2.35	0.62
2:H:231:THR:OG1	2:H:234:GLU:HG3	1.99	0.61
6:H:807:SO4:S	7:H:703:LDA:HM23	2.42	0.59
2:H:86:ARG:HH22	2:H:111:ALA:HB3	1.66	0.59
1:C:1:CYS:HB2	14:L:1204:HOH:O	2.03	0.58
6:H:807:SO4:O3	7:H:703:LDA:HM23	2.03	0.58
3:L:181:PHE:HB3	9:M:405:BPB:CBB	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:145:VAL:O	1:C:146:ARG:HD2	2.03	0.57
4:M:132:TYR:CE1	4:M:142:THR:HG21	2.39	0.56
4:M:71:PHE:HB3	7:M:705:LDA:C6	2.35	0.56
7:H:701:LDA:H52	12:M:501:MQ9:H202	1.89	0.55
3:L:182:VAL:HG11	10:L:502:UQ7:H253	1.88	0.55
4:M:95:PRO:HD3	4:M:174:PRO:HB3	1.88	0.55
9:L:406:BPB:HBB	4:M:208:TYR:CD2	2.41	0.55
2:H:30:LEU:O	2:H:34:ARG:HD2	2.07	0.55
2:H:133:LYS:HG2	2:H:134:ILE:HD12	1.89	0.55
2:H:20:GLN:HG2	4:M:202:PHE:CE2	2.42	0.54
3:L:214:GLN:HE21	4:M:19:VAL:H	1.55	0.54
4:M:112:TRP:CZ3	7:M:705:LDA:H81	2.42	0.54
4:M:162:HIS:HB3	4:M:163:PRO:HD3	1.90	0.54
2:H:139:VAL:HG21	2:H:228:ASP:HB3	1.89	0.54
2:H:6:LEU:HD12	2:H:10:LEU:HD12	1.90	0.54
3:L:135:ARG:HB3	3:L:136:PRO:HD3	1.88	0.54
8:M:403:BCB:H203	9:M:405:BPB:C4	2.38	0.54
3:L:185:MET:HE3	8:M:401:BCB:H41	1.91	0.53
7:L:702:LDA:H111	4:M:198:PRO:HA	1.91	0.52
8:M:403:BCB:H203	9:M:405:BPB:H4	1.92	0.52
2:H:22:LEU:C	2:H:22:LEU:HD13	2.35	0.51
2:H:235:GLU:OE1	4:M:231:ARG:NH2	2.38	0.51
2:H:81:ARG:N	7:H:703:LDA:H112	2.25	0.51
1:C:18:SER:HB2	3:L:156:TRP:CD1	2.47	0.50
3:L:213:ASN:OD1	10:L:502:UQ7:HM21	2.11	0.50
4:M:241:THR:O	4:M:245:ARG:HG3	2.12	0.50
4:M:160:CYS:C	4:M:163:PRO:HD2	2.37	0.50
2:H:134:ILE:HD12	2:H:134:ILE:N	2.27	0.50
4:M:146:TRP:HA	4:M:146:TRP:CE3	2.47	0.50
2:H:6:LEU:HD12	2:H:10:LEU:CD1	2.42	0.50
4:M:157:CYS:HA	4:M:161:ILE:HB	1.93	0.50
2:H:80:ARG:HA	7:H:703:LDA:H101	1.93	0.50
1:C:102:TYR:CG	1:C:103:PRO:HD3	2.47	0.49
4:M:178:TRP:HB2	4:M:179:PRO:HD3	1.94	0.49
1:C:35:ASP:OD2	1:C:316:LEU:HA	2.13	0.49
2:H:43:LEU:HB3	3:L:1:ALA:H3	1.78	0.49
4:M:298:LYS:HE3	4:M:299:HIS:NE2	2.28	0.48
2:H:216:GLU:H	2:H:216:GLU:CD	2.20	0.48
1:C:283:ALA:HB3	1:C:284:PRO:HD3	1.96	0.48
8:L:404:BCB:OBB	8:L:404:BCB:HHC	2.13	0.48
4:M:147:ASN:C	4:M:147:ASN:HD22	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:161:ASP:CG	2:H:163:VAL:HG13	2.38	0.48
3:L:246:PHE:CD1	10:L:502:UQ7:H412	2.49	0.48
1:C:111:LEU:O	1:C:115:ARG:HG3	2.14	0.48
1:C:278:ASN:HB3	1:C:302:GLN:NE2	2.29	0.47
8:L:404:BCB:HBB2	8:L:404:BCB:HMB3	1.94	0.47
10:L:502:UQ7:H171	8:M:401:BCB:C9	2.43	0.47
1:C:80:TRP:CD1	1:C:133:TYR:HB2	2.49	0.47
3:L:43:PHE:CD1	12:M:501:MQ9:H512	2.50	0.47
3:L:167:TRP:HE1	3:L:173:HIS:CD2	2.33	0.47
1:C:161:THR:OG1	1:C:164:GLU:HG3	2.15	0.47
8:L:402:BCB:H11	8:L:404:BCB:H2C	1.97	0.47
2:H:133:LYS:CG	2:H:134:ILE:HD12	2.45	0.46
3:L:197:VAL:HG13	3:L:207:LYS:HB2	1.95	0.46
4:M:107:LEU:HA	4:M:111:GLY:HA3	1.96	0.46
4:M:192:GLY:O	4:M:193:ASN:HB3	2.14	0.46
3:L:146:PHE:HB3	3:L:156:TRP:CD2	2.50	0.46
8:M:403:BCB:HMB3	8:M:403:BCB:CBB	2.46	0.46
2:H:62:LEU:O	7:H:703:LDA:HM13	2.15	0.46
8:M:401:BCB:H142	8:M:401:BCB:C10	2.45	0.46
1:C:66:THR:OG1	1:C:69:GLU:HG3	2.16	0.46
2:H:86:ARG:NH2	2:H:110:ASP:O	2.49	0.46
8:L:404:BCB:H172	9:L:406:BPB:H11A	1.98	0.46
2:H:26:THR:O	2:H:30:LEU:HB2	2.16	0.45
3:L:35:GLY:O	3:L:39:ILE:HG12	2.16	0.45
2:H:90:LEU:HD23	2:H:103:PRO:HA	1.98	0.45
13:M:600:NS5:H29	13:M:600:NS5:H271	1.82	0.45
8:M:403:BCB:HHC	8:M:403:BCB:OBB	2.17	0.45
1:C:181:ALA:O	1:C:182:TYR:HB2	2.15	0.45
2:H:56:ASP:HB3	2:H:60:TYR:CE2	2.52	0.45
8:M:401:BCB:HHC	8:M:401:BCB:CBB	2.43	0.45
4:M:112:TRP:CH2	7:M:705:LDA:H81	2.52	0.45
4:M:115[A]:MET:HA	4:M:115[A]:MET:HE3	1.99	0.45
7:L:702:LDA:H31	7:L:702:LDA:C7	2.46	0.45
1:C:102:TYR:CD2	1:C:103:PRO:HD3	2.52	0.44
3:L:17:ILE:HG13	3:L:18:GLY:N	2.32	0.44
2:H:69:VAL:CG1	3:L:204:ASP:O	2.65	0.44
4:M:34:TYR:CD1	4:M:34:TYR:N	2.85	0.44
2:H:256:SER:HA	3:L:15:THR:O	2.18	0.44
2:H:161:ASP:HB3	2:H:214:LEU:HD22	1.99	0.44
2:H:25:TRP:HA	2:H:25:TRP:CE3	2.51	0.44
8:L:402:BCB:OBB	8:L:402:BCB:HHC	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:THR:O	1:C:20:GLY:HA3	2.18	0.43
4:M:132:TYR:CZ	4:M:136:ARG:HD2	2.53	0.43
4:M:178:TRP:O	4:M:181:ILE:HB	2.18	0.43
3:L:60:ASP:OD2	7:L:702:LDA:HM12	2.19	0.43
3:L:214:GLN:HG2	4:M:19:VAL:HB	2.00	0.43
8:L:402:BCB:HMB1	8:L:402:BCB:HBB3	1.99	0.43
1:C:99:GLU:OE2	1:C:108:ARG:NH2	2.51	0.42
1:C:217:GLY:HA2	4:M:167:GLY:O	2.18	0.42
4:M:227:PHE:HB2	4:M:242:ALA:HB2	2.01	0.42
1:C:104:TYR:C	1:C:104:TYR:CD1	2.97	0.42
3:L:215:TYR:O	3:L:219:VAL:HG23	2.20	0.42
2:H:200:PHE:CZ	4:M:226:ARG:HD3	2.54	0.42
3:L:213:ASN:O	3:L:217:ARG:HG3	2.19	0.42
3:L:259:TRP:N	3:L:260:PRO:CD	2.83	0.42
6:M:804:SO4:O4	7:M:704:LDA:HM11	2.19	0.42
1:C:82:SER:HB2	1:C:85:GLU:HB2	2.01	0.42
1:C:309:HIS:CE1	1:C:315:PRO:HD3	2.55	0.42
3:L:166:ASN:OD1	3:L:168:HIS:HB2	2.19	0.42
9:L:406:BPB:CBB	4:M:208:TYR:CD2	3.02	0.42
10:L:502:UQ7:H312	10:L:502:UQ7:H352	2.02	0.42
4:M:178:TRP:N	4:M:179:PRO:CD	2.83	0.42
2:H:6:LEU:HB2	2:H:10:LEU:HD12	2.02	0.42
2:H:188:ALA:C	2:H:190:SER:H	2.28	0.42
9:M:405:BPB:HBBB	9:M:405:BPB:CHC	2.37	0.42
2:H:10:LEU:HD13	2:H:15:LEU:HD21	2.01	0.42
3:L:194:ILE:HD11	10:L:502:UQ7:HM31	2.01	0.42
4:M:159:GLY:HA3	13:M:600:NS5:H272	2.02	0.42
1:C:173:VAL:HB	4:M:87:GLN:OE1	2.19	0.41
3:L:146:PHE:HB3	3:L:156:TRP:CE3	2.55	0.41
4:M:11:GLN:OE1	4:M:39:GLY:HA3	2.21	0.41
4:M:178:TRP:HA	4:M:178:TRP:CE3	2.55	0.41
2:H:10:LEU:HB2	2:H:14:GLN:OE1	2.21	0.41
4:M:236:ILE:HG12	4:M:260:ILE:HG23	2.01	0.41
1:C:3:GLU:O	3:L:254:PHE:HA	2.20	0.41
2:H:22:LEU:HD13	2:H:22:LEU:O	2.21	0.41
4:M:2:ASP:OD1	4:M:4:GLN:HB2	2.20	0.41
13:M:600:NS5:H22	13:M:600:NS5:H7	2.02	0.41
3:L:60:ASP:HA	3:L:61:PRO:HD3	1.89	0.40
1:C:56:TYR:HB3	5:C:401:HEC:CGA	2.51	0.40
3:L:17:ILE:HG22	3:L:34:PHE:CE2	2.56	0.40
2:H:64:TYR:CZ	7:H:703:LDA:HM22	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:M:232:GLU:O	4:M:236:ILE:HG13	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	330/332 (99%)	320 (97%)	10 (3%)	0	100	100
2	H	256/258 (99%)	249 (97%)	6 (2%)	1 (0%)	30	34
3	L	272/273 (100%)	267 (98%)	4 (2%)	1 (0%)	30	34
4	M	322/323 (100%)	310 (96%)	12 (4%)	0	100	100
All	All	1180/1186 (100%)	1146 (97%)	32 (3%)	2 (0%)	43	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	55	GLU
3	L	31	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	281/281 (100%)	280 (100%)	1 (0%)	84	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	212/212 (100%)	209 (99%)	3 (1%)	59	75
3	L	219/218 (100%)	216 (99%)	3 (1%)	59	75
4	M	250/249 (100%)	247 (99%)	3 (1%)	63	78
All	All	962/960 (100%)	952 (99%)	10 (1%)	68	81

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	152	LEU
2	H	69	VAL
2	H	163	VAL
2	H	236	ASP
3	L	16	LEU
3	L	80	LEU
3	L	119	LEU
4	M	147	ASN
4	M	194	PHE
4	M	214	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	54	GLN
1	C	58	ASN
1	C	94	ASN
1	C	95	ASN
1	C	127	GLN
1	C	206	GLN
2	H	8	GLN
2	H	58	GLN
2	H	178	HIS
3	L	214	GLN
3	L	239	ASN
4	M	147	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	FME	H	1	2	8,9,10	0.66	0	8,9,11	2.16	2 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FME	H	1	2	-	1/7/9/11	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	FME	CA-N-CN	-4.17	116.40	122.82
2	H	1	FME	O1-CN-N	-3.95	115.12	125.32

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	1	FME	O1-CN-N-CA

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 27 ligands modelled in this entry, 1 is monoatomic - leaving 26 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	HEC	C	403	1	50,50,50	1.03	3 (6%)	68,82,82	1.03	5 (7%)
7	LDA	M	705	-	13,15,15	2.70	2 (15%)	14,17,17	0.53	0
10	UQ7	L	502	-	48,48,48	1.69	10 (20%)	60,61,61	1.20	7 (11%)
6	SO4	M	801	-	4,4,4	0.47	0	6,6,6	0.24	0
7	LDA	M	704	-	13,15,15	2.67	2 (15%)	14,17,17	0.56	0
8	BCB	L	402	3	68,74,74	1.24	7 (10%)	77,115,115	1.83	10 (12%)
7	LDA	H	703	-	13,15,15	2.20	2 (15%)	14,17,17	0.52	0
9	BPB	M	405	-	57,70,70	1.65	10 (17%)	55,101,101	2.25	12 (21%)
8	BCB	M	401	4	68,74,74	1.30	8 (11%)	77,115,115	1.81	7 (9%)
8	BCB	M	403	4	68,74,74	1.23	7 (10%)	77,115,115	1.83	10 (12%)
6	SO4	M	803	-	4,4,4	0.52	0	6,6,6	0.43	0
8	BCB	L	404	3	68,74,74	1.46	8 (11%)	77,115,115	2.30	11 (14%)
7	LDA	L	702	-	13,15,15	2.57	2 (15%)	14,17,17	0.52	0
7	LDA	H	701	-	13,15,15	2.28	2 (15%)	14,17,17	0.52	0
6	SO4	H	807	-	4,4,4	0.54	0	6,6,6	0.31	0
6	SO4	M	804	-	4,4,4	0.46	0	6,6,6	0.28	0
9	BPB	L	406	-	57,70,70	1.69	9 (15%)	55,101,101	2.28	12 (21%)
5	HEC	C	401	1	50,50,50	1.03	4 (8%)	68,82,82	1.10	5 (7%)
5	HEC	C	404	1	50,50,50	1.02	3 (6%)	68,82,82	1.09	7 (10%)
13	NS5	M	600	-	39,39,39	0.46	0	46,46,46	0.91	4 (8%)
5	HEC	C	402	1	50,50,50	1.06	4 (8%)	68,82,82	1.11	6 (8%)
6	SO4	H	806	-	4,4,4	0.35	0	6,6,6	0.18	0
12	MQ9	M	501	-	59,59,59	1.58	11 (18%)	73,75,75	1.03	5 (6%)
6	SO4	M	805	-	4,4,4	0.42	0	6,6,6	0.35	0
6	SO4	H	802	-	4,4,4	0.38	0	6,6,6	0.15	0
7	LDA	L	706	-	13,15,15	2.57	2 (15%)	14,17,17	0.58	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	HEC	C	403	1	1/1/3/7	7/14/54/54	-
7	LDA	M	705	-	-	0/13/13/13	-
10	UQ7	L	502	-	-	13/45/69/69	0/1/1/1
7	LDA	M	704	-	-	0/13/13/13	-
8	BCB	L	402	3	3/3/21/26	6/41/137/137	-
7	LDA	H	703	-	-	0/13/13/13	-
9	BPB	M	405	-	2/2/18/23	3/37/105/105	0/5/6/6
8	BCB	M	401	4	4/4/21/26	7/41/137/137	-
8	BCB	M	403	4	3/3/21/26	4/41/137/137	-
8	BCB	L	404	3	2/2/21/26	3/41/137/137	-
7	LDA	L	702	-	-	2/13/13/13	-
7	LDA	H	701	-	-	1/13/13/13	-
9	BPB	L	406	-	-	2/37/105/105	0/5/6/6
5	HEC	C	401	1	1/1/3/7	6/14/54/54	-
5	HEC	C	404	1	1/1/3/7	5/14/54/54	-
13	NS5	M	600	-	-	14/43/43/43	-
5	HEC	C	402	1	1/1/3/7	8/14/54/54	-
12	MQ9	M	501	-	-	4/53/73/73	0/2/2/2
7	LDA	L	706	-	-	1/13/13/13	-

All (96) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	705	LDA	O1-N1	-7.99	1.22	1.42
7	M	704	LDA	O1-N1	-7.82	1.23	1.42
7	L	702	LDA	O1-N1	-7.77	1.23	1.42
7	L	706	LDA	O1-N1	-7.59	1.23	1.42
7	H	703	LDA	O1-N1	-7.37	1.24	1.42
7	H	701	LDA	O1-N1	-6.96	1.25	1.42
7	M	704	LDA	C1-N1	-5.57	1.45	1.51
7	M	705	LDA	C1-N1	-5.54	1.45	1.51
8	L	404	BCB	MG-NA	5.50	2.19	2.06
9	L	406	BPB	C1D-C2D	5.40	1.45	1.39
9	M	405	BPB	C1D-C2D	5.32	1.45	1.39
7	L	706	LDA	C1-N1	-5.28	1.46	1.51
8	M	401	BCB	MG-NA	5.19	2.18	2.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	M	403	BCB	MG-NA	5.17	2.18	2.06
9	M	405	BPB	C3A-C2A	-5.09	1.50	1.54
7	L	702	LDA	C1-N1	-5.02	1.46	1.51
9	L	406	BPB	C3A-C2A	-4.77	1.50	1.54
8	L	404	BCB	O2A-CGA	4.77	1.47	1.33
8	L	402	BCB	MG-NA	4.63	2.17	2.06
9	M	405	BPB	C1B-C2B	4.58	1.44	1.39
7	H	701	LDA	C1-N1	-4.34	1.47	1.51
9	L	406	BPB	C1B-C2B	4.33	1.44	1.39
9	L	406	BPB	C3B-C4B	3.91	1.47	1.41
9	L	406	BPB	O2D-CGD	3.73	1.42	1.33
8	L	402	BCB	O2D-CGD	3.61	1.42	1.33
8	L	404	BCB	C1-C2	-3.54	1.39	1.49
8	L	404	BCB	O2D-CGD	3.52	1.41	1.33
9	M	405	BPB	C3B-C4B	3.51	1.47	1.41
8	M	401	BCB	O2D-CGD	3.44	1.41	1.33
10	L	502	UQ7	C7-C8	-3.43	1.45	1.50
9	M	405	BPB	O2D-CGD	3.25	1.41	1.33
5	C	404	HEC	FE-NB	3.24	2.04	1.94
8	L	404	BCB	O2D-CED	-3.16	1.38	1.45
5	C	401	HEC	FE-NB	3.15	2.04	1.94
5	C	402	HEC	FE-NB	3.06	2.04	1.94
8	M	401	BCB	O2A-CGA	3.04	1.42	1.33
8	M	403	BCB	O2D-CGD	3.00	1.40	1.33
9	L	406	BPB	O2A-CGA	2.96	1.42	1.33
8	M	401	BCB	O2D-CED	-2.95	1.38	1.45
8	L	404	BCB	C3B-C4B	2.93	1.46	1.41
10	L	502	UQ7	C13-C14	2.93	1.39	1.33
8	M	403	BCB	C3B-C4B	2.93	1.46	1.41
8	M	403	BCB	MG-ND	-2.93	2.00	2.05
8	M	401	BCB	C3B-C4B	2.92	1.46	1.41
12	M	501	MQ9	C43-C44	2.91	1.39	1.33
12	M	501	MQ9	C33-C34	2.90	1.39	1.33
9	L	406	BPB	C2-C3	2.88	1.39	1.33
10	L	502	UQ7	O3-CM3	-2.86	1.38	1.45
10	L	502	UQ7	C33-C34	2.86	1.39	1.33
8	L	402	BCB	MG-ND	-2.86	2.00	2.05
10	L	502	UQ7	C8-C9	2.85	1.39	1.33
5	C	403	HEC	FE-ND	2.85	2.03	1.94
12	M	501	MQ9	C28-C29	2.84	1.39	1.33
10	L	502	UQ7	C28-C29	2.83	1.39	1.33
10	L	502	UQ7	C23-C24	2.82	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	L	502	UQ7	C18-C19	2.81	1.39	1.33
7	H	703	LDA	C1-N1	-2.77	1.48	1.51
8	L	402	BCB	C3B-C4B	2.77	1.46	1.41
12	M	501	MQ9	C38-C39	2.76	1.39	1.33
12	M	501	MQ9	C8-C9	2.73	1.39	1.33
9	M	405	BPB	O2A-CGA	2.72	1.41	1.33
12	M	501	MQ9	C23-C24	2.68	1.39	1.33
8	M	403	BCB	C2-C3	2.67	1.39	1.33
9	M	405	BPB	C2-C3	2.61	1.39	1.33
12	M	501	MQ9	C18-C19	2.61	1.39	1.33
8	L	404	BCB	C2-C3	2.60	1.39	1.33
8	M	401	BCB	C1-C2	-2.60	1.41	1.49
8	M	401	BCB	C2-C3	2.56	1.39	1.33
10	L	502	UQ7	O2-CM2	-2.53	1.39	1.45
5	C	401	HEC	FE-ND	2.52	2.02	1.94
5	C	404	HEC	FE-NA	2.52	2.03	1.95
12	M	501	MQ9	C13-C14	2.50	1.38	1.33
9	L	406	BPB	C3B-C2B	-2.48	1.35	1.39
5	C	401	HEC	FE-NC	2.47	2.03	1.95
8	L	402	BCB	C1-C2	-2.47	1.42	1.49
10	L	502	UQ7	C38-C39	2.47	1.39	1.32
5	C	402	HEC	FE-NC	2.43	2.03	1.95
12	M	501	MQ9	C48-C49	2.40	1.39	1.32
9	M	405	BPB	C3B-C2B	-2.40	1.35	1.39
5	C	402	HEC	FE-NA	2.39	2.03	1.95
8	L	402	BCB	C2-C3	2.37	1.38	1.33
8	M	403	BCB	O2A-CGA	2.35	1.40	1.33
5	C	404	HEC	FE-NC	2.34	2.02	1.95
9	L	406	BPB	O2D-CED	-2.33	1.40	1.45
9	M	405	BPB	O2D-CED	-2.33	1.40	1.45
8	M	403	BCB	O2D-CED	-2.29	1.40	1.45
9	M	405	BPB	CHA-CBD	2.23	1.54	1.51
5	C	403	HEC	FE-NC	2.22	2.02	1.95
12	M	501	MQ9	C32-C33	-2.22	1.43	1.50
8	L	402	BCB	O2D-CED	-2.16	1.40	1.45
8	L	404	BCB	CAC-C3C	2.15	1.38	1.33
5	C	402	HEC	FE-ND	2.11	2.01	1.94
5	C	401	HEC	FE-NA	2.09	2.02	1.95
5	C	403	HEC	FE-NB	2.09	2.01	1.94
8	M	401	BCB	C3B-C2B	-2.02	1.35	1.42
12	M	501	MQ9	C36-C34	2.01	1.55	1.51

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	M	405	BPB	O2D-CGD-CBD	10.83	122.85	110.95
9	L	406	BPB	O2D-CGD-CBD	10.67	122.67	110.95
8	L	404	BCB	C1-C2-C3	10.28	143.04	126.20
8	M	403	BCB	C4A-NA-C1A	9.07	110.82	106.68
8	L	404	BCB	C4A-NA-C1A	8.73	110.66	106.68
8	M	401	BCB	C4A-NA-C1A	8.66	110.63	106.68
8	L	402	BCB	C4A-NA-C1A	8.66	110.63	106.68
8	L	404	BCB	O2D-CGD-CBD	6.66	122.88	111.23
8	M	401	BCB	O2D-CGD-CBD	6.56	122.70	111.23
9	M	405	BPB	O1D-CGD-CBD	-6.29	115.18	124.72
9	L	406	BPB	O1D-CGD-CBD	-6.28	115.20	124.72
8	M	403	BCB	O2D-CGD-CBD	6.08	121.86	111.23
9	M	405	BPB	C4D-CHA-CBD	-5.47	105.83	108.45
8	L	402	BCB	O2D-CGD-CBD	5.40	120.67	111.23
8	L	402	BCB	C1C-NC-C4C	5.24	109.07	106.68
8	L	404	BCB	C1C-NC-C4C	5.19	109.05	106.68
8	M	403	BCB	C1C-NC-C4C	5.06	108.99	106.68
8	L	404	BCB	C5-C3-C2	5.02	132.43	121.17
9	L	406	BPB	C4D-CHA-CBD	-4.88	106.11	108.45
8	M	401	BCB	O1D-CGD-CBD	-4.84	114.98	124.52
8	M	401	BCB	C1C-NC-C4C	4.79	108.87	106.68
8	L	404	BCB	O1D-CGD-CBD	-4.74	115.17	124.52
5	C	401	HEC	CAB-C3B-C4B	-4.58	118.82	124.79
8	L	404	BCB	C4-C3-C2	-4.42	112.27	123.63
8	M	403	BCB	O1D-CGD-CBD	-4.38	115.88	124.52
9	L	406	BPB	C1-C2-C3	4.34	133.30	126.20
8	L	402	BCB	O1D-CGD-CBD	-4.16	116.31	124.52
5	C	403	HEC	CAC-C3C-C2C	4.01	133.23	126.89
5	C	403	HEC	CAC-C3C-C4C	-3.84	119.64	124.91
5	C	402	HEC	CAC-C3C-C2C	3.75	132.82	126.89
8	L	402	BCB	O2A-CGA-CBA	3.72	123.18	111.83
5	C	401	HEC	CAB-C3B-C2B	3.63	134.22	127.56
5	C	402	HEC	CAC-C3C-C4C	-3.59	119.98	124.91
5	C	404	HEC	CAB-C3B-C4B	-3.51	120.22	124.79
9	M	405	BPB	OBD-CAD-CBD	-3.49	120.71	125.82
9	L	406	BPB	OBD-CAD-CBD	-3.32	120.94	125.82
12	M	501	MQ9	C37-C38-C39	3.30	135.17	127.62
9	L	406	BPB	O2A-CGA-CBA	3.24	121.72	111.83
5	C	404	HEC	CAC-C3C-C2C	3.17	131.90	126.89
5	C	403	HEC	CAB-C3B-C4B	-3.16	120.67	124.79
5	C	402	HEC	CAB-C3B-C4B	-3.15	120.69	124.79
8	M	403	BCB	OBB-CAB-C3B	3.15	126.00	120.43
8	L	402	BCB	O2A-CGA-O1A	-3.09	115.90	123.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	M	405	BPB	C4D-ND-C1D	-3.02	105.25	108.87
9	L	406	BPB	C4D-ND-C1D	-2.98	105.30	108.87
10	L	502	UQ7	C17-C18-C19	2.92	134.31	127.62
5	C	404	HEC	CAC-C3C-C4C	-2.88	120.95	124.91
8	L	404	BCB	O2A-CGA-CBA	2.86	120.56	111.83
5	C	404	HEC	CAB-C3B-C2B	2.86	132.81	127.56
5	C	401	HEC	CAC-C3C-C2C	2.83	131.36	126.89
8	L	402	BCB	OBB-CAB-C3B	2.74	125.27	120.43
12	M	501	MQ9	C32-C33-C34	2.72	133.85	127.62
8	M	403	BCB	C2A-C1A-CHA	2.70	128.56	123.87
10	L	502	UQ7	C12-C11-C9	-2.67	104.32	113.19
12	M	501	MQ9	C7-C6-C5	-2.66	120.33	124.89
8	L	402	BCB	C2A-C1A-CHA	2.65	128.47	123.87
5	C	403	HEC	CAB-C3B-C2B	2.60	132.33	127.56
5	C	402	HEC	CAB-C3B-C2B	2.59	132.31	127.56
9	L	406	BPB	C3D-C4D-ND	2.56	110.99	107.71
10	L	502	UQ7	C7-C6-C5	-2.53	120.55	124.89
8	M	403	BCB	CAB-C3B-C2B	2.52	132.98	127.74
9	L	406	BPB	O2A-CGA-O1A	-2.51	117.36	123.63
5	C	401	HEC	CAC-C3C-C4C	-2.48	121.50	124.91
9	M	405	BPB	C3D-C4D-ND	2.47	110.87	107.71
8	L	402	BCB	CAB-C3B-C2B	2.45	132.84	127.74
13	M	600	NS5	C19-C18-C17	2.45	128.53	123.52
12	M	501	MQ9	C7-C8-C9	2.43	131.02	126.83
9	L	406	BPB	C2D-C1D-ND	2.41	111.17	109.43
10	L	502	UQ7	C25-C24-C26	-2.41	111.04	115.23
8	L	404	BCB	CAB-C3B-C2B	2.40	132.73	127.74
9	M	405	BPB	O2A-CGA-CBA	2.38	119.10	111.83
8	M	403	BCB	O2A-CGA-CBA	2.36	119.03	111.83
13	M	600	NS5	C16-C15-C14	-2.34	114.51	118.09
9	M	405	BPB	C4B-NB-C1B	-2.31	105.44	108.82
9	M	405	BPB	C5-C3-C2	2.28	126.28	121.17
5	C	404	HEC	CBD-CAD-C3D	2.26	118.78	112.53
8	L	404	BCB	OBB-CAB-C3B	2.26	124.43	120.43
5	C	403	HEC	CMB-C2B-C1B	2.19	128.46	125.03
9	M	405	BPB	C2D-C1D-ND	2.17	111.00	109.43
13	M	600	NS5	C13-C12-C10	2.17	130.74	127.69
5	C	404	HEC	CAA-C2A-C3A	-2.17	123.81	127.87
8	M	403	BCB	CMB-C2B-C1B	-2.16	122.13	125.42
8	L	404	BCB	CED-O2D-CGD	2.16	120.81	115.92
10	L	502	UQ7	CM3-O3-C3	2.14	124.01	116.47
5	C	402	HEC	CMD-C2D-C1D	2.14	128.38	125.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	502	UQ7	C7-C8-C9	2.14	130.51	126.83
13	M	600	NS5	C19-C20-C21	-2.14	124.28	127.28
12	M	501	MQ9	C45-C44-C46	-2.13	111.53	115.23
8	M	401	BCB	C15-C13-C12	2.13	122.86	112.07
10	L	502	UQ7	C37-C36-C34	2.13	120.24	113.19
5	C	404	HEC	CAA-C2A-C1A	2.12	129.16	124.85
9	M	405	BPB	CMA-C3A-C4A	-2.10	110.08	114.61
8	M	401	BCB	C6-C5-C3	2.09	118.57	113.47
9	L	406	BPB	OBD-CAD-C3D	2.09	131.15	127.89
9	M	405	BPB	OBD-CAD-C3D	2.08	131.13	127.89
8	M	403	BCB	CBB-CAB-C3B	-2.06	116.05	120.40
5	C	401	HEC	CMD-C2D-C1D	2.05	128.24	125.03
9	L	406	BPB	CMA-C3A-C4A	-2.04	110.22	114.61
8	M	401	BCB	C1-C2-C3	2.03	129.53	126.20
5	C	402	HEC	CBD-CAD-C3D	2.03	118.14	112.53
8	L	402	BCB	CED-O2D-CGD	2.01	120.48	115.92

All (18) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	C	401	HEC	NA
5	C	402	HEC	NA
5	C	403	HEC	NA
5	C	404	HEC	NA
8	L	402	BCB	NC
8	L	402	BCB	ND
8	L	402	BCB	NA
8	L	404	BCB	NC
8	L	404	BCB	NA
8	M	401	BCB	C8
8	M	401	BCB	NC
8	M	401	BCB	ND
8	M	401	BCB	NA
8	M	403	BCB	NC
8	M	403	BCB	ND
8	M	403	BCB	NA
9	M	405	BPB	C13
9	M	405	BPB	C8

All (86) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	M	403	BCB	CAD-CBD-CGD-O1D
8	M	403	BCB	CAD-CBD-CGD-O2D
13	M	600	NS5	C13-C14-C15-C16
10	L	502	UQ7	C31-C32-C33-C34
10	L	502	UQ7	C19-C21-C22-C23
8	L	404	BCB	CBA-CGA-O2A-C1
8	L	402	BCB	C4-C3-C5-C6
10	L	502	UQ7	C30-C29-C31-C32
8	L	402	BCB	C2-C3-C5-C6
10	L	502	UQ7	C28-C29-C31-C32
5	C	401	HEC	C2B-C3B-CAB-CBB
13	M	600	NS5	C22-C21-C23-C24
8	L	404	BCB	O1A-CGA-O2A-C1
5	C	402	HEC	C2B-C3B-CAB-CBB
5	C	403	HEC	C2B-C3B-CAB-CBB
8	M	403	BCB	C2A-CAA-CBA-CGA
5	C	404	HEC	C2B-C3B-CAB-CBB
8	M	401	BCB	C4B-C3B-CAB-CBB
5	C	403	HEC	C4C-C3C-CAC-CBC
8	L	404	BCB	C2-C1-O2A-CGA
13	M	600	NS5	C34-C35-C36-CM4
5	C	403	HEC	C2C-C3C-CAC-CBC
5	C	402	HEC	C4B-C3B-CAB-CBB
8	L	402	BCB	C15-C16-C17-C18
5	C	401	HEC	C4C-C3C-CAC-CBC
5	C	401	HEC	C2C-C3C-CAC-CBC
13	M	600	NS5	C3-C4-C5-C7
5	C	401	HEC	C4B-C3B-CAB-CBB
9	M	405	BPB	CBA-CGA-O2A-C1
5	C	403	HEC	C4B-C3B-CAB-CBB
9	L	406	BPB	O2A-C1-C2-C3
7	L	702	LDA	N1-C1-C2-C3
5	C	404	HEC	C2C-C3C-CAC-CBC
5	C	404	HEC	C4B-C3B-CAB-CBB
10	L	502	UQ7	C15-C14-C16-C17
8	M	401	BCB	C11-C12-C13-C15
9	M	405	BPB	O1A-CGA-O2A-C1
13	M	600	NS5	C3-C4-C5-C6
7	L	702	LDA	C3-C4-C5-C6
10	L	502	UQ7	C13-C14-C16-C17
13	M	600	NS5	C11-C10-C12-C13
10	L	502	UQ7	C25-C24-C26-C27
13	M	600	NS5	C7-C8-C9-C10

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Mol	Chain	Res	Type	Atoms
5	C	402	HEC	C2C-C3C-CAC-CBC
8	M	401	BCB	C2B-C3B-CAB-CBB
7	L	706	LDA	C7-C8-C9-C10
10	L	502	UQ7	C20-C19-C21-C22
10	L	502	UQ7	C23-C24-C26-C27
9	L	406	BPB	C4C-C3C-CAC-CBC
5	C	402	HEC	C4C-C3C-CAC-CBC
8	L	402	BCB	C16-C17-C18-C20
5	C	404	HEC	C4C-C3C-CAC-CBC
13	M	600	NS5	C20-C21-C23-C24
8	M	401	BCB	C4B-C3B-CAB-OB
10	L	502	UQ7	C18-C19-C21-C22
8	L	402	BCB	CAD-CBD-CGD-O2D
8	L	402	BCB	CAD-CBD-CGD-O1D
8	M	401	BCB	C3-C5-C6-C7
5	C	404	HEC	C2D-C3D-CAD-CBD
13	M	600	NS5	C32-C31-C33-C34
13	M	600	NS5	C2-C3-C4-C5
10	L	502	UQ7	C35-C34-C36-C37
8	M	401	BCB	C2B-C3B-CAB-OB
5	C	401	HEC	CAA-CBA-CGA-O2A
10	L	502	UQ7	C33-C34-C36-C37
5	C	401	HEC	CAA-CBA-CGA-O1A
12	M	501	MQ9	C45-C44-C46-C47
13	M	600	NS5	C30-C31-C33-C34
5	C	402	HEC	CAD-CBD-CGD-O2D
12	M	501	MQ9	C35-C34-C36-C37
5	C	403	HEC	CAD-CBD-CGD-O2D
8	M	401	BCB	C4-C3-C5-C6
12	M	501	MQ9	C40-C39-C41-C42
13	M	600	NS5	C12-C10-C9-C8
8	M	403	BCB	O2A-C1-C2-C3
5	C	403	HEC	CAD-CBD-CGD-O1D
5	C	402	HEC	CAD-CBD-CGD-O1D
5	C	402	HEC	CAA-CBA-CGA-O2A
5	C	402	HEC	CAA-CBA-CGA-O1A
13	M	600	NS5	C13-C14-C15-C17
7	H	701	LDA	C4-C5-C6-C7
9	M	405	BPB	C6-C7-C8-C10
13	M	600	NS5	C6-C5-C7-C8
12	M	501	MQ9	C46-C47-C48-C49
10	L	502	UQ7	C12-C11-C9-C10

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Mol	Chain	Res	Type	Atoms
5	C	403	HEC	CAA-CBA-CGA-O2A

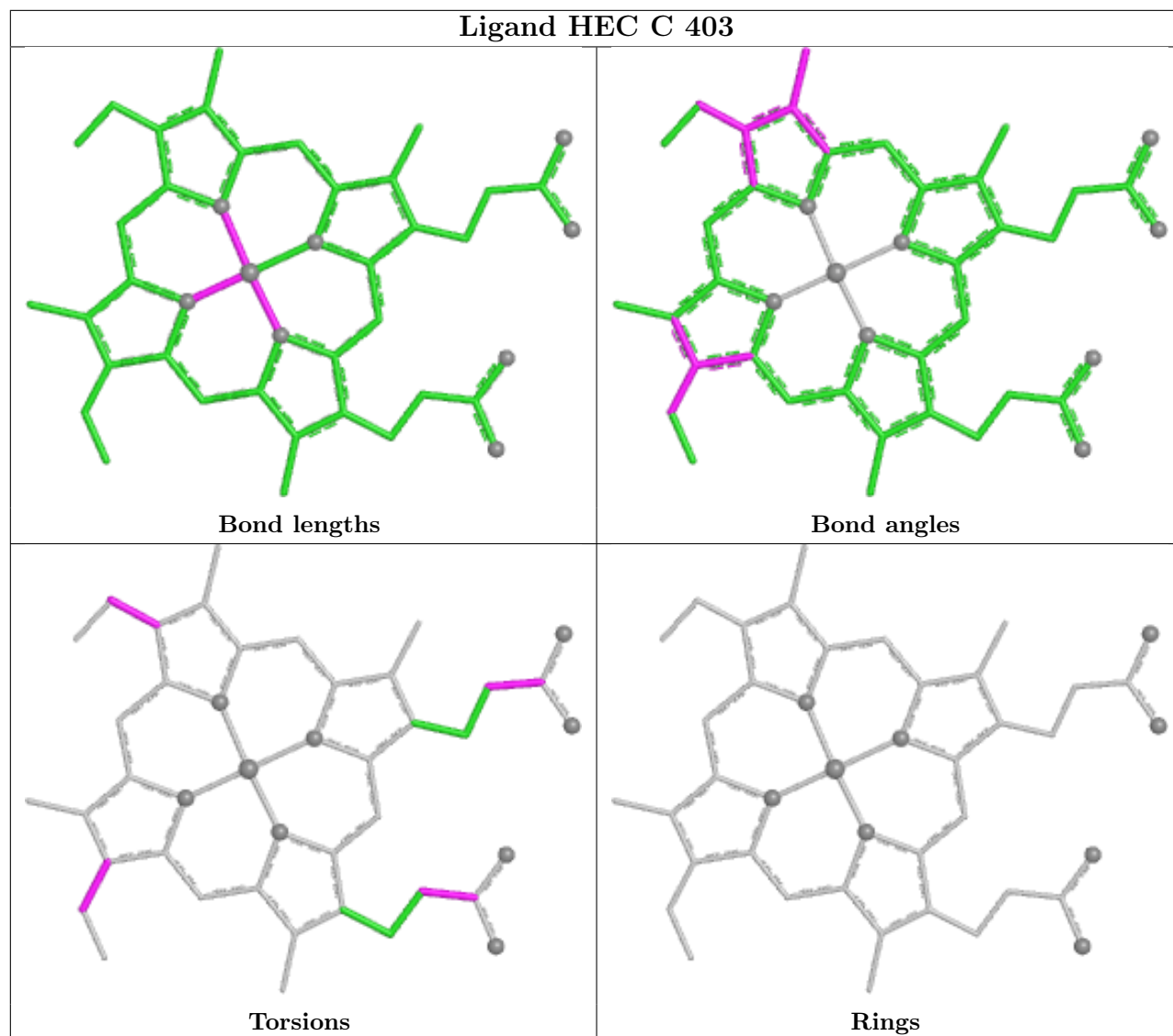
There are no ring outliers.

17 monomers are involved in 57 short contacts:

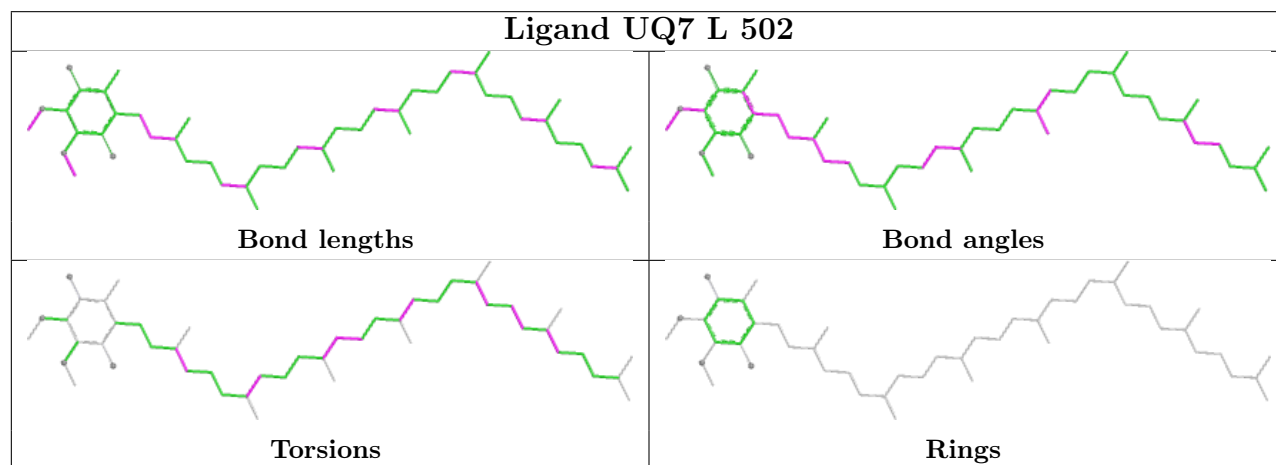
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	M	705	LDA	4	0
10	L	502	UQ7	9	0
7	M	704	LDA	1	0
8	L	402	BCB	3	0
7	H	703	LDA	7	0
9	M	405	BPB	7	0
8	M	401	BCB	8	0
8	M	403	BCB	4	0
8	L	404	BCB	4	0
7	L	702	LDA	4	0
7	H	701	LDA	1	0
6	H	807	SO4	2	0
6	M	804	SO4	1	0
9	L	406	BPB	6	0
5	C	401	HEC	1	0
13	M	600	NS5	4	0
12	M	501	MQ9	2	0

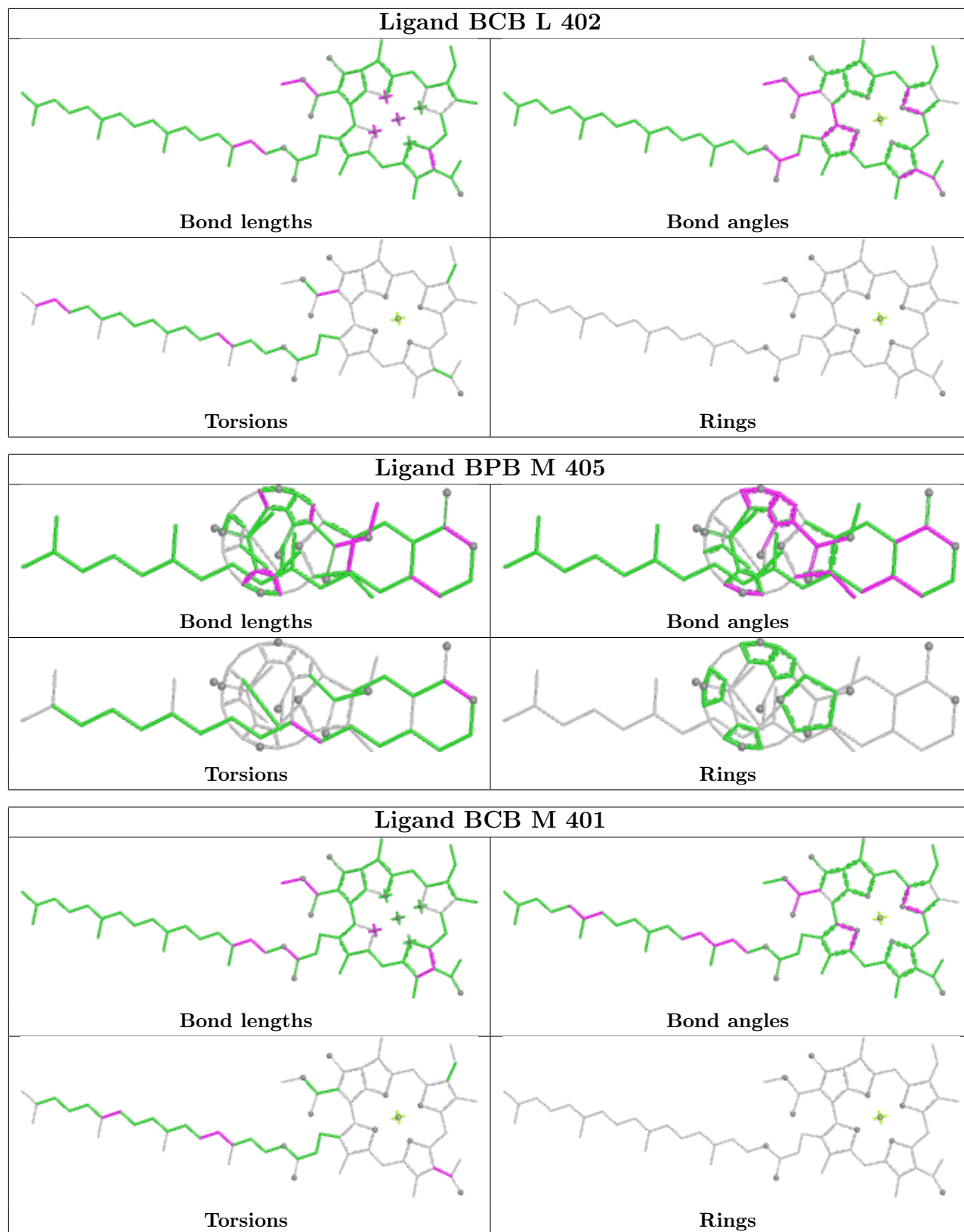
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

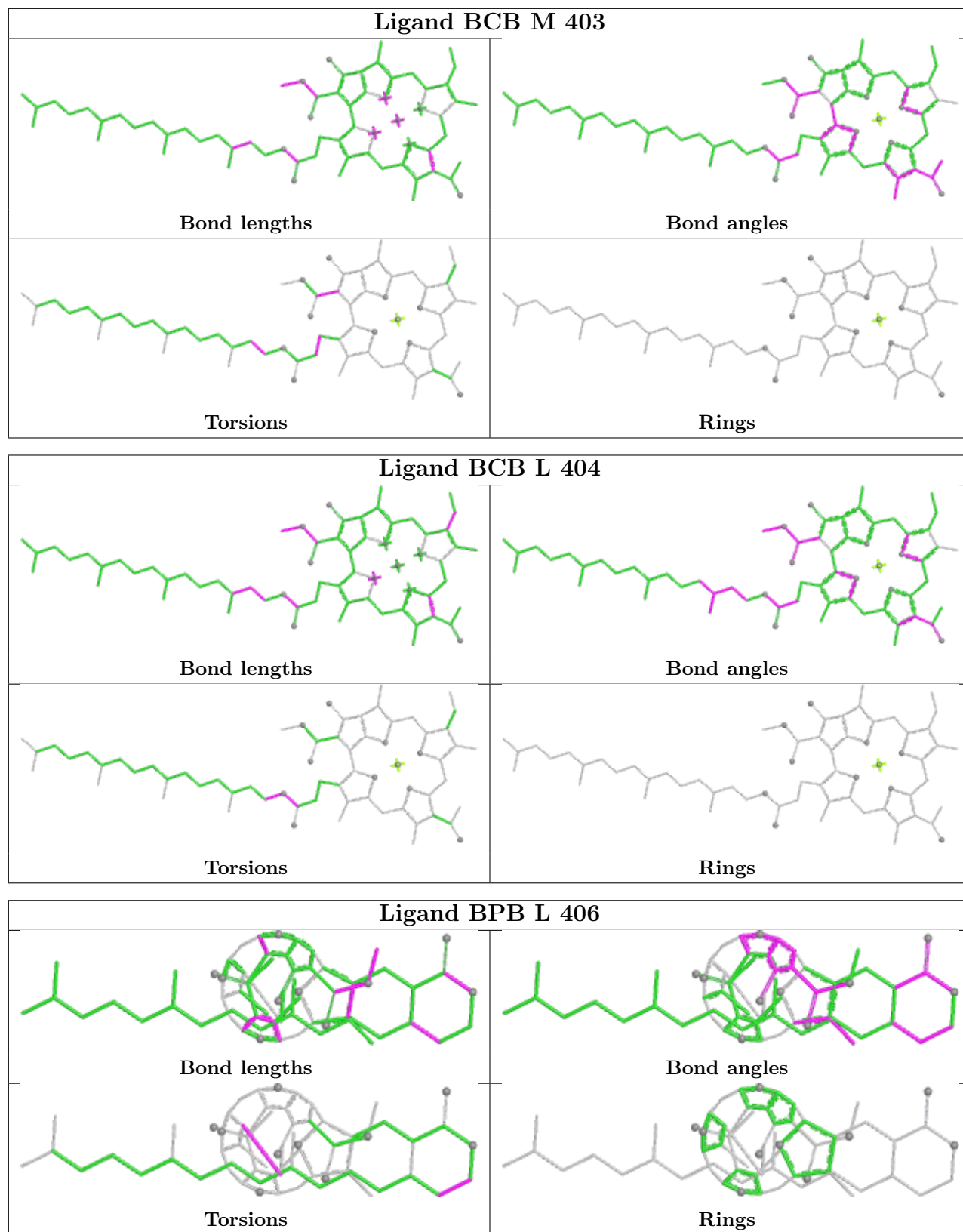
Ligand HEC C 403



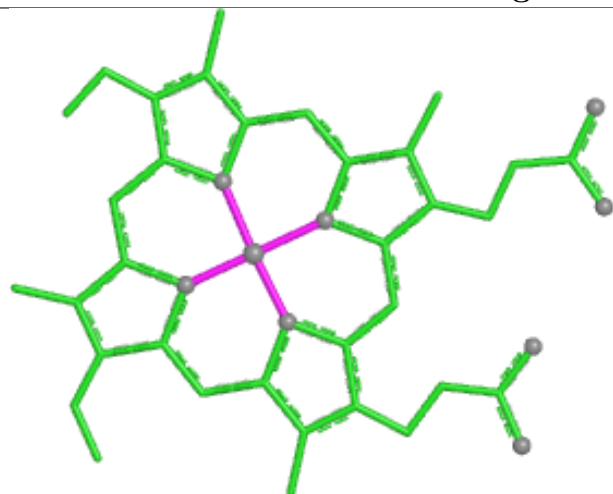
Ligand UQ7 L 502



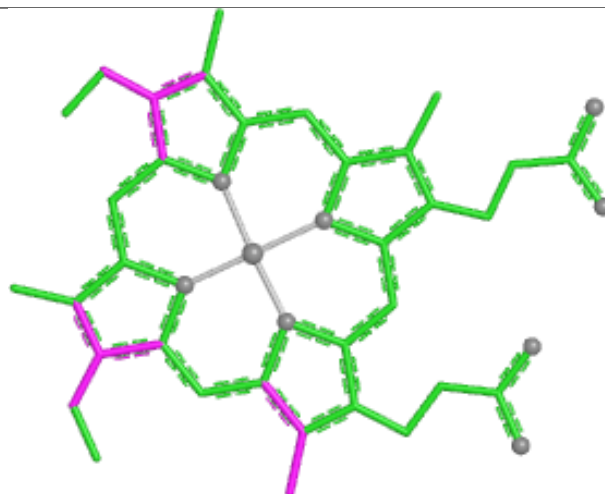




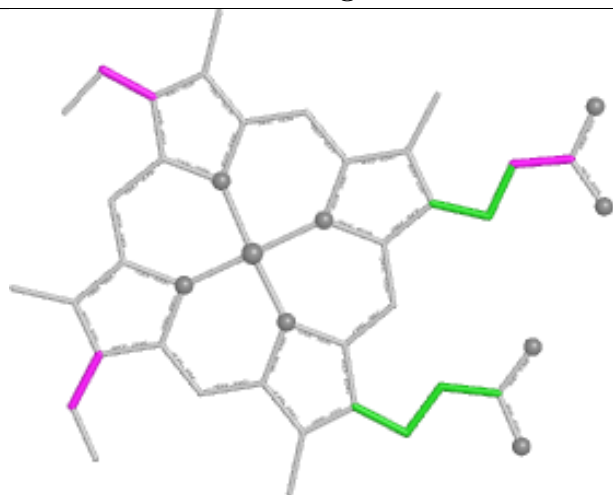
Ligand HEC C 401



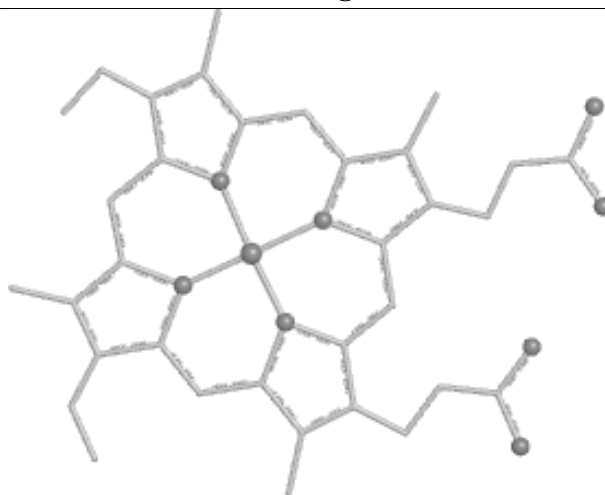
Bond lengths



Bond angles

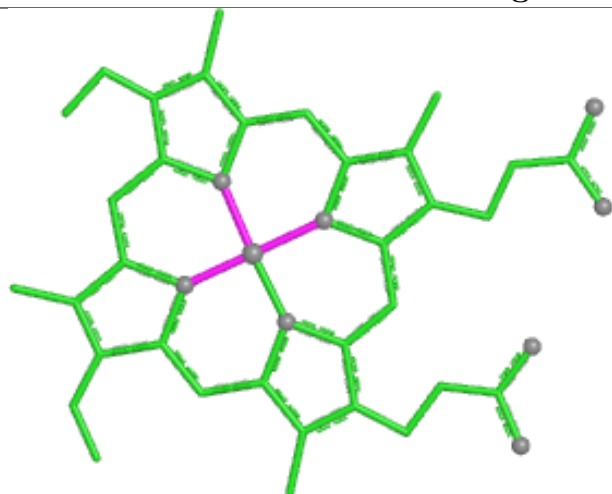


Torsions

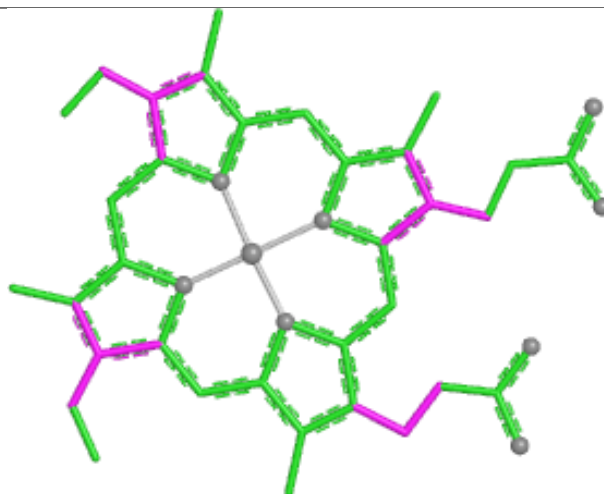


Rings

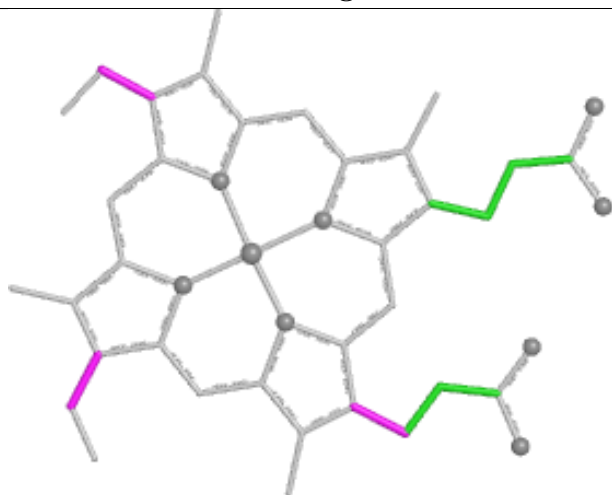
Ligand HEC C 404



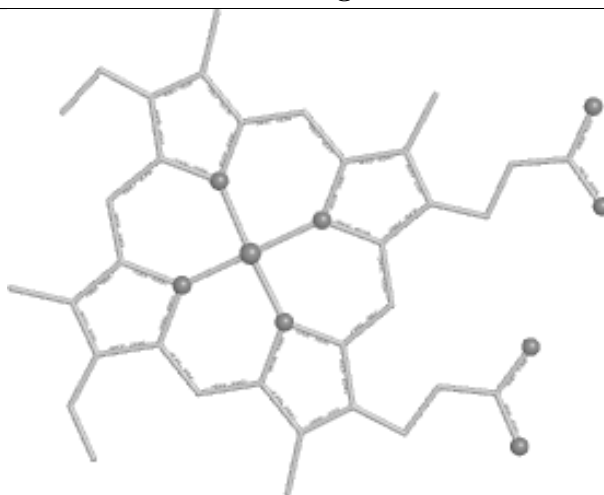
Bond lengths



Bond angles

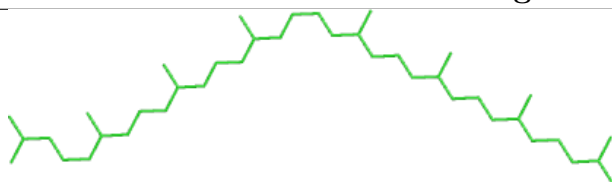


Torsions

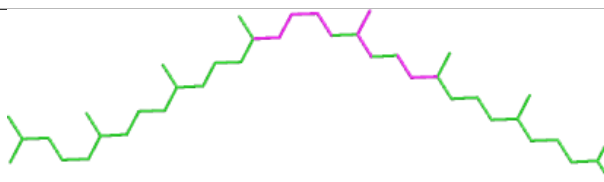


Rings

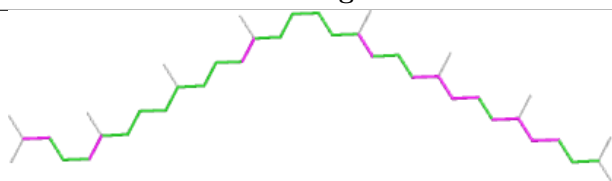
Ligand NS5 M 600



Bond lengths



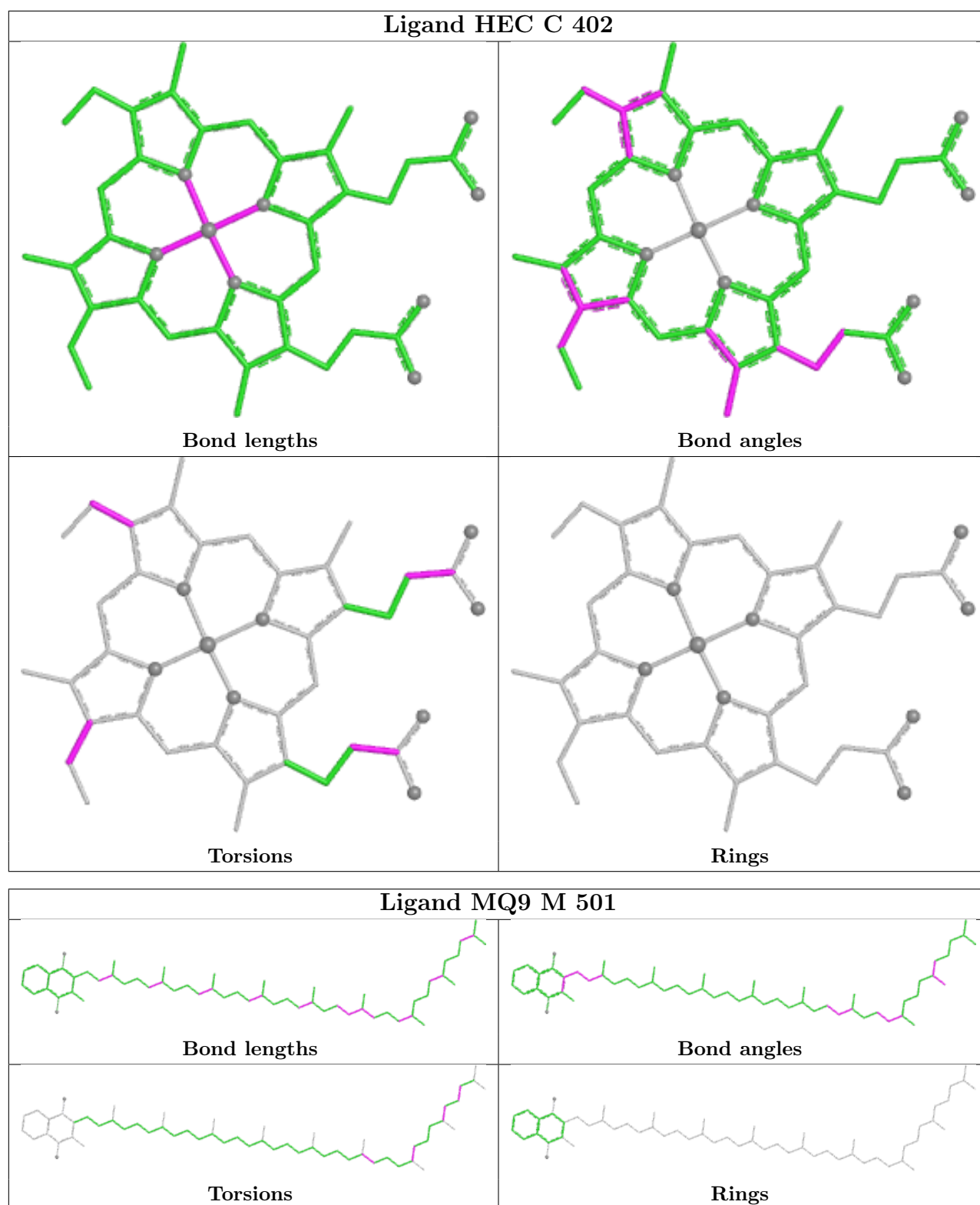
Bond angles



Torsions



Rings



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	C	332/332 (100%)	0.03	10 (3%) 52 49	16, 27, 42, 59	9 (2%)
2	H	248/258 (96%)	0.54	27 (10%) 10 8	16, 31, 46, 57	20 (8%)
3	L	273/273 (100%)	-0.22	5 (1%) 67 64	6, 23, 35, 52	5 (1%)
4	M	323/323 (100%)	0.02	14 (4%) 40 36	11, 26, 43, 58	7 (2%)
All	All	1176/1186 (99%)	0.08	56 (4%) 35 32	6, 27, 43, 59	41 (3%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	45	GLU	9.1
2	H	96	PHE	4.3
2	H	85	THR	4.2
2	H	9	HIS	4.1
2	H	95	GLY	4.1
2	H	191	ALA	4.0
2	H	190	SER	3.8
4	M	30	GLY	3.7
1	C	1	CYS	3.6
2	H	8	GLN	3.5
2	H	10	LEU	3.5
2	H	193	THR	3.4
4	M	115[A]	MET	3.4
4	M	108	HIS	3.4
3	L	202	ASP	3.4
2	H	94	ASP	3.2
3	L	271	PHE	3.1
2	H	206	ASP	3.1
3	L	1	ALA	3.1
2	H	83	PRO	3.1
1	C	94	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	159	THR	3.0
4	M	32	PRO	3.0
3	L	51	TYR	2.9
2	H	87	GLU	2.9
4	M	71	PHE	2.8
4	M	27	ASP	2.7
2	H	162	GLY	2.7
2	H	166	GLY	2.7
3	L	141[A]	SER	2.6
1	C	48	GLU	2.6
2	H	7	ALA	2.6
2	H	216	GLU	2.5
4	M	146	TRP	2.5
1	C	56	TYR	2.5
4	M	26	ASN	2.4
2	H	148	GLY	2.3
1	C	169	ARG	2.3
2	H	43	LEU	2.3
4	M	67	LEU	2.3
1	C	54	GLN	2.2
1	C	127	GLN	2.2
2	H	155	LEU	2.2
2	H	55	GLU	2.2
2	H	188	ALA	2.2
2	H	150	VAL	2.2
4	M	23	TRP	2.2
2	H	163	VAL	2.2
4	M	29	VAL	2.1
2	H	102	GLN	2.1
4	M	319	PRO	2.1
2	H	141	THR	2.1
1	C	46	LYS	2.0
4	M	34	TYR	2.0
1	C	50	PRO	2.0
4	M	49	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FME	H	1	10/11	0.89	0.12	28,32,49,55	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

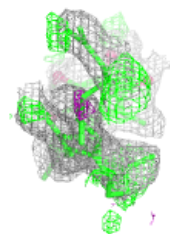
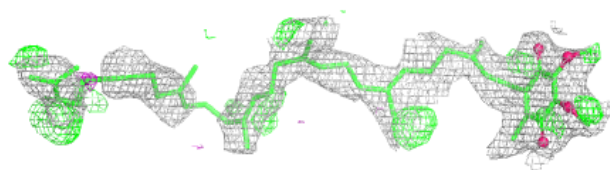
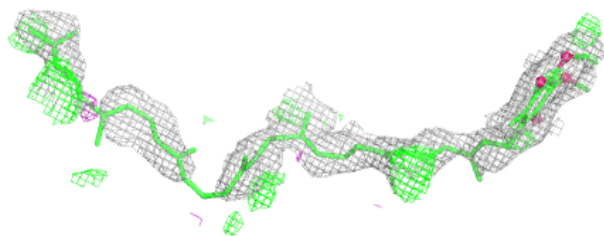
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	LDA	L	706	16/16	0.62	0.24	48,58,69,69	0
7	LDA	H	703	16/16	0.74	0.23	38,48,61,62	0
7	LDA	M	705	16/16	0.77	0.22	57,60,62,63	4
10	UQ7	L	502	48/48	0.77	0.20	23,36,44,44	48
6	SO4	H	807	5/5	0.86	0.24	31,32,32,38	5
7	LDA	H	701	16/16	0.87	0.14	23,36,50,52	0
6	SO4	M	805	5/5	0.88	0.18	55,57,59,60	0
7	LDA	M	704	16/16	0.88	0.18	52,54,65,65	0
13	NS5	M	600	40/40	0.88	0.13	24,35,65,66	0
6	SO4	H	806	5/5	0.90	0.22	58,61,63,63	0
7	LDA	L	702	16/16	0.91	0.13	29,50,54,54	0
6	SO4	M	803	5/5	0.92	0.16	46,47,53,55	0
8	BCB	M	401	66/66	0.93	0.11	15,22,68,71	0
9	BPB	M	405	65/65	0.94	0.09	14,24,57,59	9
6	SO4	H	802	5/5	0.95	0.12	57,59,60,61	0
8	BCB	L	404	66/66	0.95	0.07	10,16,41,48	0
8	BCB	L	402	66/66	0.96	0.07	13,17,23,30	0
8	BCB	M	403	66/66	0.96	0.07	12,18,40,41	0
12	MQ9	M	501	58/58	0.96	0.08	15,20,62,64	0
9	BPB	L	406	65/65	0.96	0.06	14,18,23,26	0
5	HEC	C	402	43/43	0.97	0.08	18,27,32,34	0
6	SO4	M	804	5/5	0.97	0.07	40,41,42,44	0
5	HEC	C	401	43/43	0.97	0.08	23,30,37,39	0
5	HEC	C	404	43/43	0.98	0.07	14,21,33,43	0
5	HEC	C	403	43/43	0.98	0.06	14,19,22,26	0
6	SO4	M	801	5/5	0.98	0.07	31,32,33,38	0
11	FE2	M	500	1/1	1.00	0.03	17,17,17,17	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

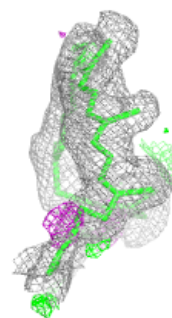
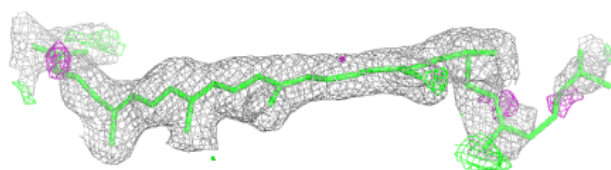
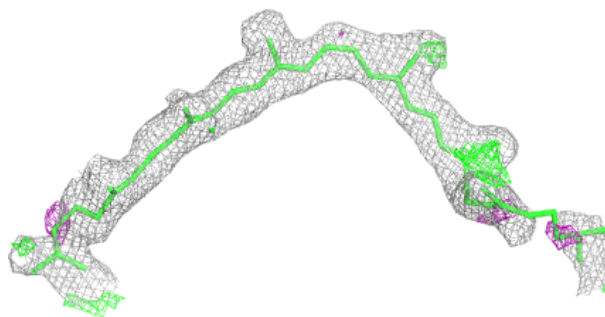
Electron density around UQ7 L 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

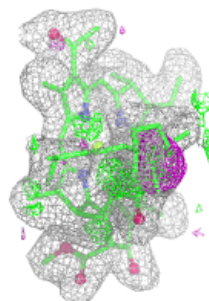
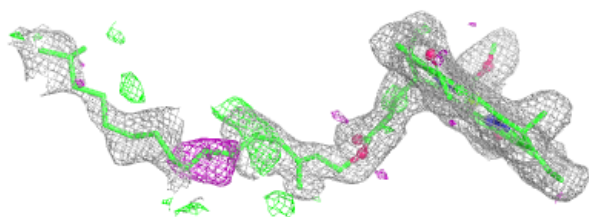
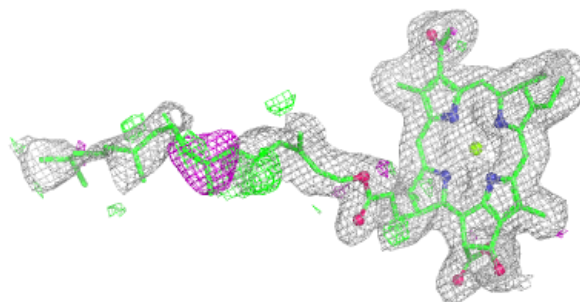


Electron density around NS5 M 600:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

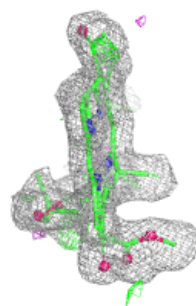
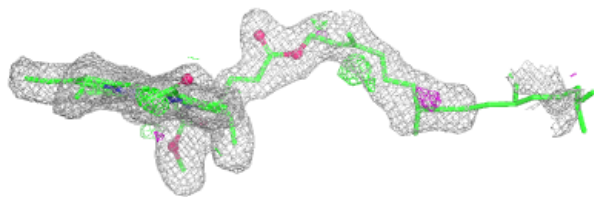
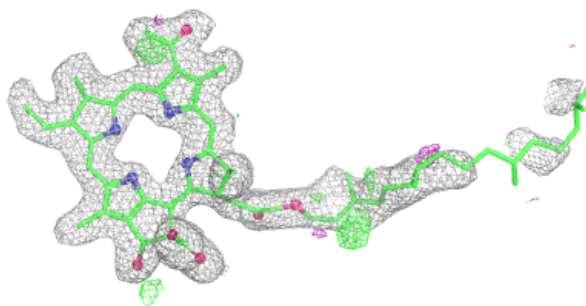
**Electron density around BCB M 401:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



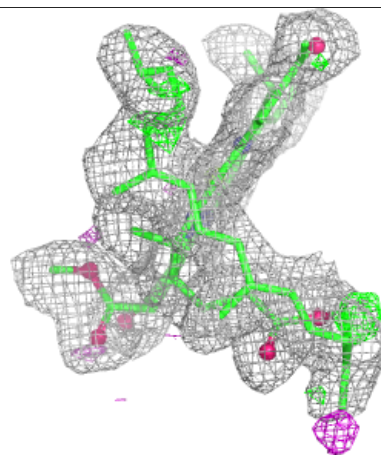
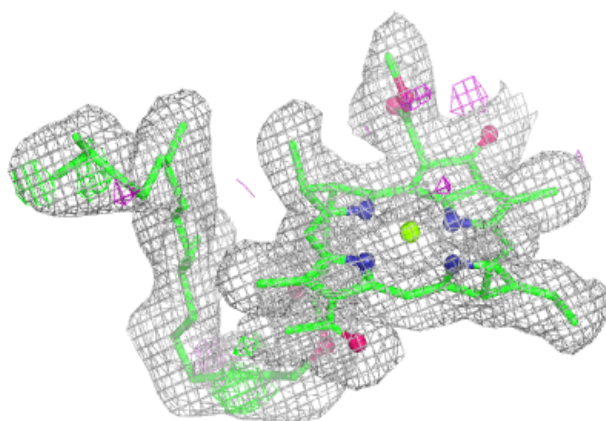
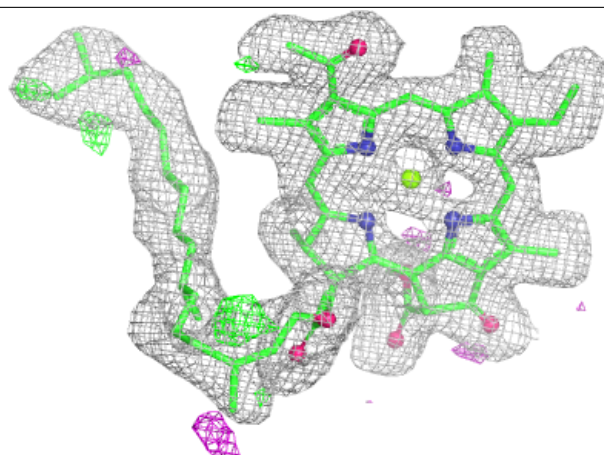
Electron density around BPB M 405:

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and green (positive)



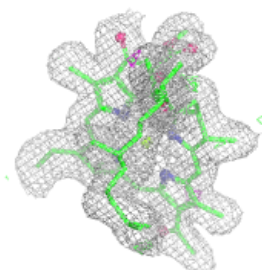
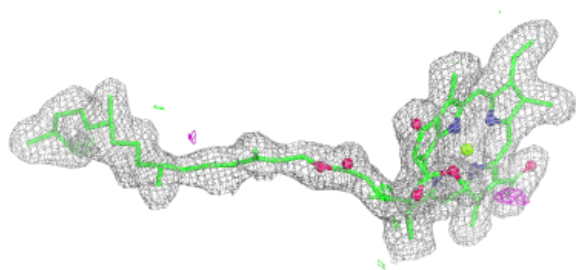
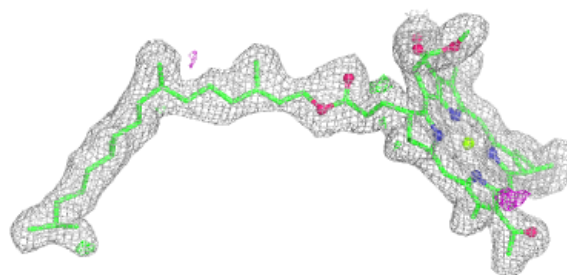
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and green (positive)

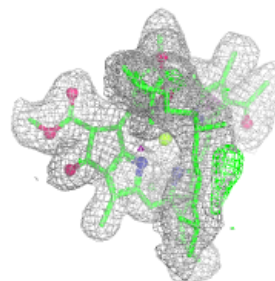
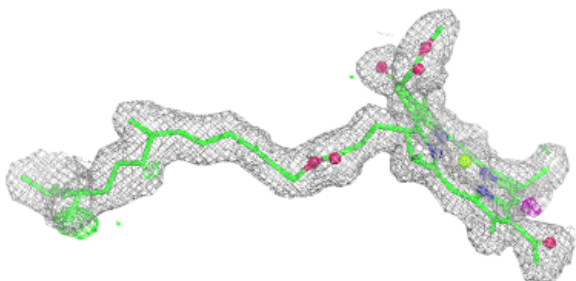
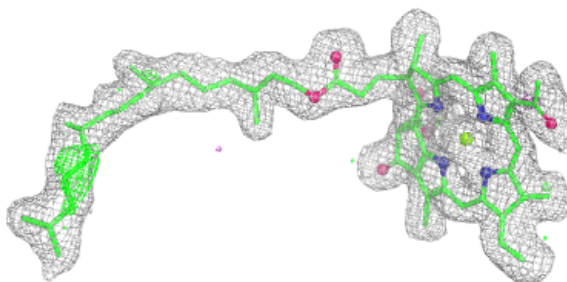


Electron density around BCB L 402:

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and green (positive)

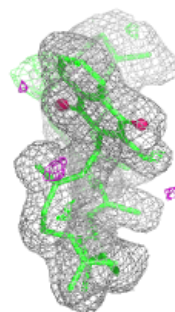
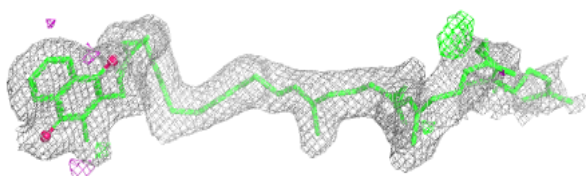
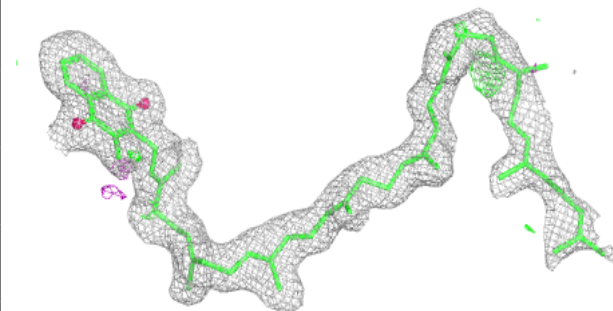
**Electron density around BCB M 403:**

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and green (positive)

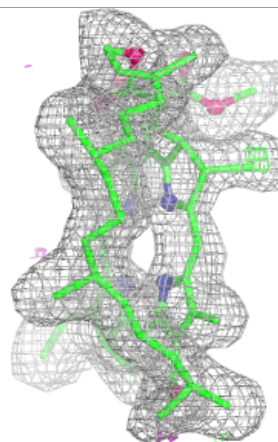
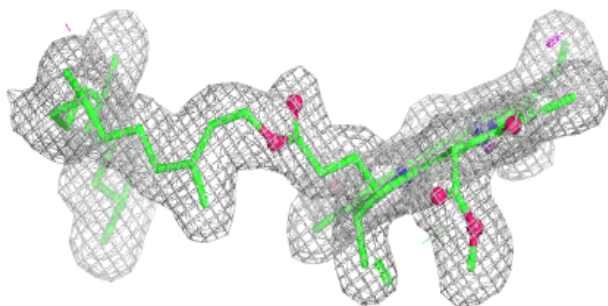
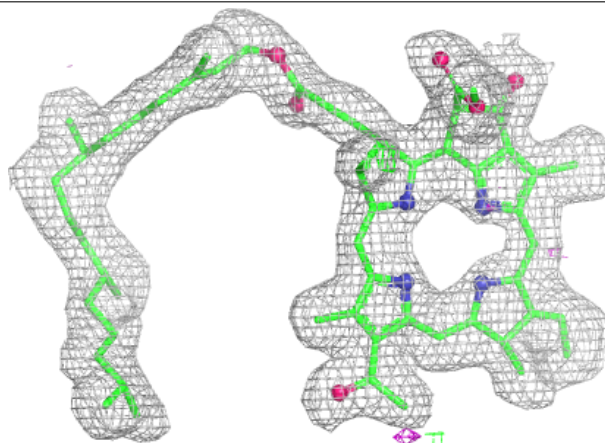


Electron density around MQ9 M 501:

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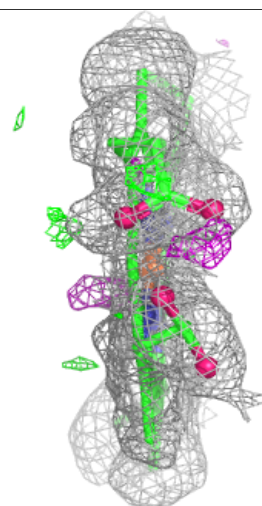
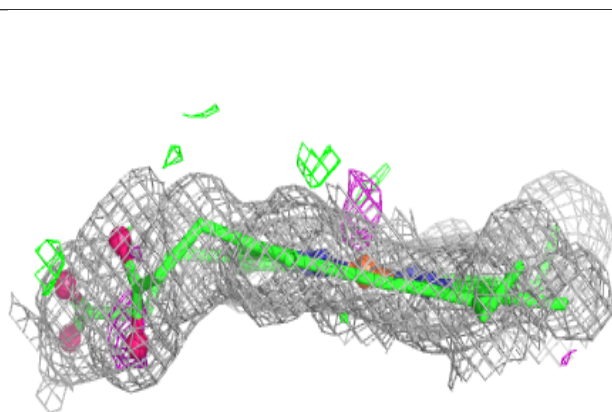
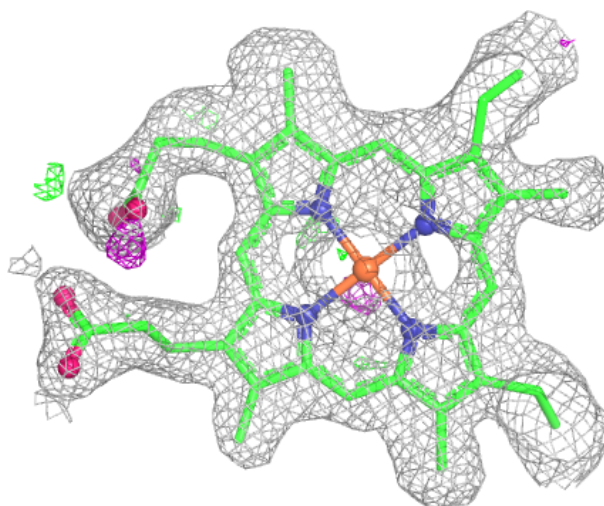
**Electron density around BPB L 406:**

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and green (positive)



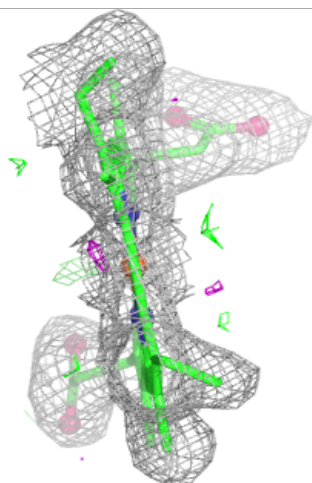
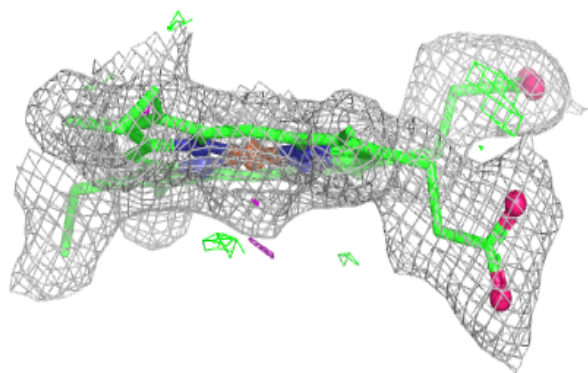
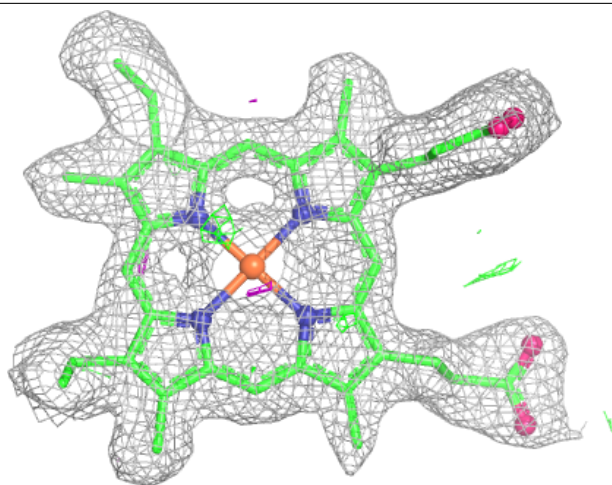
Electron density around HEC C 402:

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and green (positive)



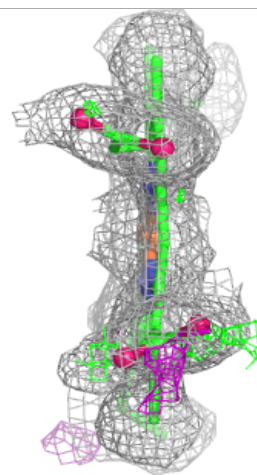
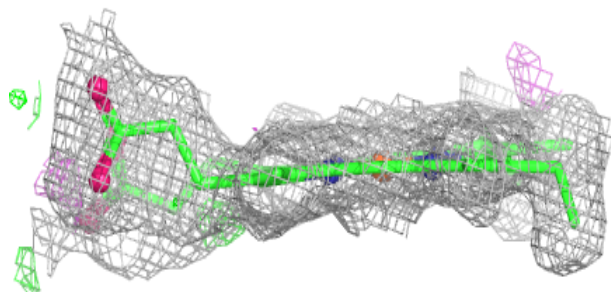
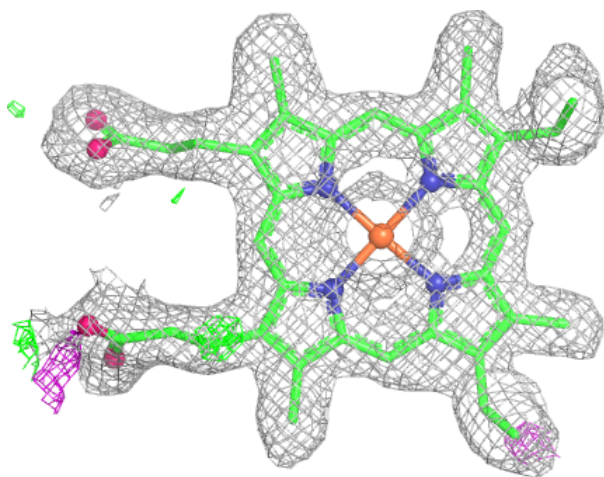
Electron density around HEC C 401:

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and green (positive)



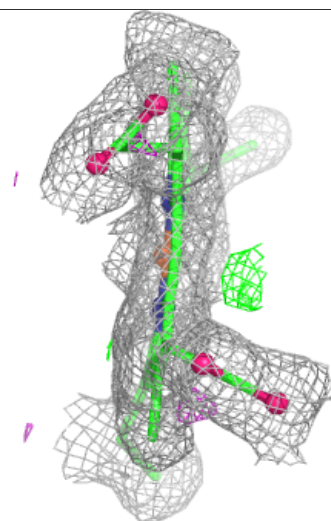
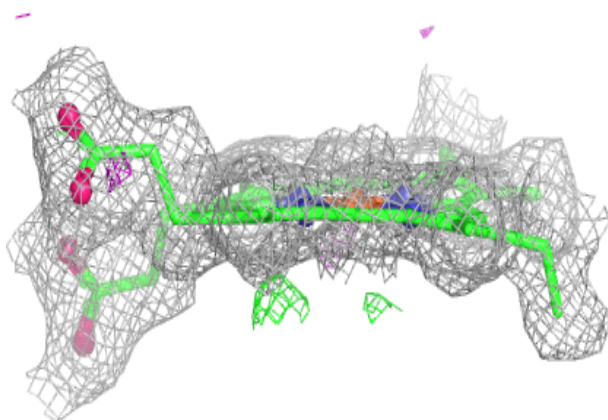
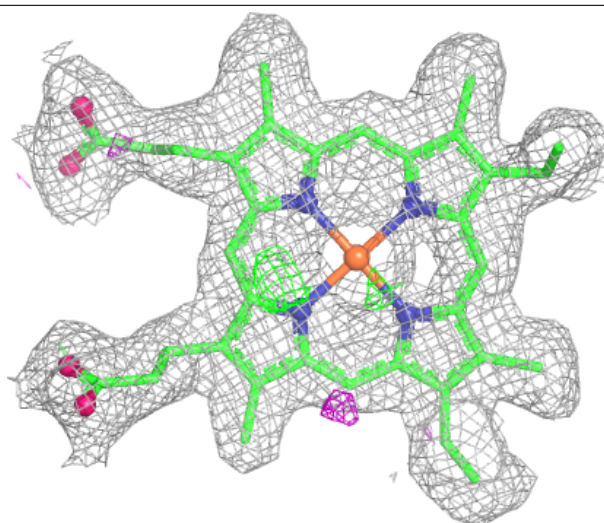
Electron density around HEC C 404:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC C 403:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.